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OM protein - protein search, using sw model

Run on: March 23, 2005, 18:59:31 ; Search time 169 Seconds
(without alignments)
469.147 Million cell updates/sec

Title: US-10-087-190-3
Perfect score: 1047
Sequence: 1 MSKKKGLSAEKRTFMELF.....FEENKIDRFGIPEDFDYID 205

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp19808:*
2: geneseqp19908:*
3: geneseqp20008:*
4: geneseqp20018:*
5: geneseqp20028:*
6: geneseqp20038:*
7: geneseqp20038:*
8: geneseqp20048:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1047	100.0	205	7	ADD84537 121P1F1 P
2	1047	100.0	205	8	ADJ70015
3	1047	100.0	205	8	ADM83851 Human can
4	1047	100.0	205	8	ADM83810 Human can
5	1047	100.0	205	8	ADM83812 Human can
6	1047	100.0	205	8	ADM83793 Human can
7	1047	100.0	205	8	ADM83811 Human can
8	1047	100.0	205	8	ADM83804 Human can
9	1047	100.0	219	6	ABP75541 Human sec
10	1036.5	99.0	206	8	ADM83834 Human can
11	1036.5	99.0	206	8	ADM83835 Human can
12	1011	96.6	198	8	ADM83814 Human can
13	975	93.1	190	4	AA440043 Human can
14	975	93.1	190	7	ADD84547 121P1F1 v
15	975	93.1	190	8	ADM83857 Human can
16	975	93.1	190	8	ADM83859 Human can
17	975	93.1	190	8	ADM83803 Human can
18	975	93.1	190	8	ADM83809 Human can
19	975	93.1	190	8	ADM83858 Human can
20	948	90.3	205	8	ADM83813 Mouse hyp
21	945.5	90.3	190	7	ADD84545 121P1F1 v
22	945.5	90.3	190	8	ADM83808 Human can
23	945.5	90.3	190	8	ADM83801 Human can
24	945.5	90.3	190	8	ADM83853 Human can
25	945.5	90.3	190	8	ADM83852 Human can

26	614	58.6	122	8	ADM83843	ADM83843 Human can
27	606	57.9	122	4	AA441829	AA441829 Human pol
28	591	56.4	122	7	ADD84543	ADD84543 121P1F1 v
29	591	56.4	122	8	ADM83799	ADM83799 Human can
30	591	56.4	122	8	ADM83845	ADM83845 Human can
31	591	56.4	122	8	ADM83807	ADM83807 Human can
32	591	56.4	122	8	ADM83844	ADM83844 Human can
33	584	55.8	119	7	ADD84541	ADD84541 121P1F1 v
34	584	55.8	119	8	ADM83797	ADM83797 Human can
35	584	55.8	119	8	ADM83806	ADM83806 Human can
36	584	55.8	119	8	ADM83837	ADM83837 Human can
37	465	44.4	126	7	ADD84539	ADD84539 121P1F1 v
38	465	44.4	126	8	ADM83836	ADM83836 Human can
39	465	44.4	126	8	ADM83795	ADM83795 Human can
40	465	44.4	126	8	ADM83805	ADM83805 Human can
41	349	33.3	200	8	ADM83815	ADM83815 Yeast hyp
42	329.5	31.5	182	4	ABG12341	ABG12341 Novel hum
43	287	27.4	79	4	AG74669	AG74669 Yeast smc
44	255.5	24.4	218	5	ADH32846	ADH32846 Yeast smc
45	135.5	12.9	1281	8	ADP26646	ADP26646 Mouse dyn

ALIGNMENTS

RESULT 1
ADD84537
ID ADD84537 standard; protein; 205 AA.
XX
XX ADD84537;
AC
AC
DT 29-JAN-2004 (first entry)
DT
XX
DE 121P1F1 protein.
XX
XX 121P1F1; 121P1F1 modulation; human; chromosome 4q; cytosolic;
KM gene therapy; vaccine; cancer; immune response; immunisation.
XX
XX Homo sapiens.
OS
XX
XX WO200295009-A2.
PN
XX
PD 28-NOV-2002.
PD
XX
PF 28-FEB-2002; 2002WO-US006242.
PF
XX
PR 05-MAR-2001; 2001US-00799250.
PR
XX
XX (AGEN-) AGENSYS INC.
PA
XX
XX Challa-Bid PM, Hubert RS, Raitano AB, Faris M, Afar DEH, Ge W;
PI Jakovovits A;
PI
XX
DR WPI; 2003-156757/15.
DR
XX
XX N-PSDB; ADD84536.
XX
PT Composition comprising a substance that modulates the status of 121P1F1,
PT useful in diagnosing, preventing, prognosticating or treating patients
PT with cancer that expresses 121P1F1, such as breast, colon, ovarian or
PT lung cancer.
PT
PS Claim 19; Fig 2A; 2855p; English.
PS
XX
XX The present invention describes a composition (I) comprising a substance
XX that modulates the status of 121P1F1 (gene and encoded protein), or a
XX molecule that is modulated by 121P1F1, where the status of a cell that
XX expresses 121P1F1 is modulated. The human 121P1F1 gene maps to chromosome
XX 4q. (I) has cytosolic activity, and can be used in gene therapy, and in
XX vaccines. The composition (I) can be used for diagnosing, preventing,
XX prognosticating or treating patients with cancer that expresses 121P1F1,
XX such as breast, colon, ovarian or lung cancer. The 121P1F1 gene or its
XX fragment can be used to elicit a humoral or cellular immune response.
XX 121P1F1 antibodies can be used in active or passive immunisation. 121P1F1

CC polynucleotides are useful as probes and primers for the amplification or
 CC detection of 121P1 genes, as coding sequences for directing the
 CC expression of 121P1 polypeptides, or as tools for modulating or
 CC inhibiting the expression of 121P1 genes. The present sequence is used
 CC in the exemplification of the present invention.
 SQ Sequence 205 AA;

Query Match 100.0%; Score 1047; DB 7; Length 205;
 Best Local Similarity 100.0%; Pred. No. 1.5e-88;
 Matches 205; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSKKKGLSAEKKRTMMEIFSETKDVFOLEKIAPEKKGITAMSVKVEVQSLVDDGMV 60
 DB 1 MSKKKGLSAEKKRTMMEIFSETKDVFOLEKIAPEKKGITAMSVKVEVQSLVDDGMV 60
 QY 61 DCERIGTSNYMAFPSPKALHARKHKLVEVLSQSLSGSQKASLOKSIKAKIGRCETEE 120
 DB 61 DCERIGTSNYMAFPSPKALHARKHKLVEVLSQSLSGSQKASLOKSIKAKIGRCETEE 120
 QY 121 TRLAKELSLRDQREQLKAEVEKYDCDPQVEEIRQANKVAKAANRWTDNIFAKSWA 180
 DB 121 TRLAKELSLRDQREQLKAEVEKYDCDPQVEEIRQANKVAKAANRWTDNIFAKSWA 180
 QY 181 KRKFGFEENKIDRTGTGIPEDFDYID 205
 DB 181 KRKFGFEENKIDRTGTGIPEDFDYID 205

RESULT 2
 ADJ70015
 ID ADJ70015 standard; protein; 205 AA.
 AC ADJ70015;
 XX
 DT 06-MAY-2004 (first entry)
 XX

DE Human heat mitochondrial protein as a therapeutic target SeqID1821.
 XX
 KW mitochondrial; human; screening assay; diabetes mellitus;
 KW Huntington's disease; osteoarthritis;
 KW Leber's hereditary optic neuropathy; LHON;
 KW mitochondrial encephalopathy lactic acidosis and stroke; MELAS;
 KW myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;
 KW neuroprotective; nootropic; antidiabetic; anticonvulsant; antiarthritic;
 KW osteopathic; ophthalmological; cytostatic.
 OS Homo sapiens.
 XX
 PN WO2003087768-A2.
 XX
 PD 23-OCT-2003.
 XX
 PF 04-APR-2003; 2003WO-US010870.
 XX
 PR 12-APR-2002; 2002US-0372843P.
 PR 17-JUN-2002; 2002US-038987P.
 PR 20-SEP-2002; 2002US-0412418P.
 XX
 PA (MITO-) MITOKOR
 PA (BUCK-) BUCK INST AGE RES.
 XX
 PI Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GM;
 PI Warnock DE;
 XX
 DR WPI; 2003-845369/78.
 XX

Identifying a mitochondrial target for drug screening assays and for
 PT treating diseases associated with altered mitochondrial function,
 PT comprises detecting a modified polypeptide in a sample and correlating
 PT with the disease.
 XX
 PS Claim 1; SEQ ID NO 1821; 180pp; English.

XX This invention relates to novel mitochondrial targets that can be used
 CC for therapeutic intervention in treating a disease associated with
 CC altered mitochondrial function. Specifically, it refers to a method for
 CC identifying proteins of the human heart mitochondrial proteome that are
 CC useful for drug screening assays, as well as therapeutic targets. The
 CC present invention describes a method for identifying such proteins that
 CC can be used in the treatment of various diseases associated with that
 CC mitochondrial function including diabetes mellitus, Huntington's disease,
 CC osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial
 CC encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy
 CC ragged red fibre syndrome (MERRF) or cancer. Accordingly, these
 CC compositions have neuroprotective, nootropic, antidiabetic,
 CC anticonvulsant, antiarthritic, osteopathic, ophthalmological and
 CC cyostatic activities. This polypeptide sequence is a human heart
 CC mitochondrial protein of the invention.
 SQ Sequence 205 AA;

Query Match 100.0%; Score 1047; DB 7; Length 205;
 Best Local Similarity 100.0%; Pred. No. 1.5e-88;
 Matches 205; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSKKKGLSAEKKRTMMEIFSETKDVFOLEKIAPEKKGITAMSVKVEVQSLVDDGMV 60
 DB 1 MSKKKGLSAEKKRTMMEIFSETKDVFOLEKIAPEKKGITAMSVKVEVQSLVDDGMV 60
 QY 61 DCERIGTSNYMAFPSPKALHARKHKLVEVLSQSLSGSQKASLOKSIKAKIGRCETEE 120
 DB 61 DCERIGTSNYMAFPSPKALHARKHKLVEVLSQSLSGSQKASLOKSIKAKIGRCETEE 120
 QY 121 TRLAKELSLRDQREQLKAEVEKYDCDPQVEEIRQANKVAKAANRWTDNIFAKSWA 180
 DB 121 TRLAKELSLRDQREQLKAEVEKYDCDPQVEEIRQANKVAKAANRWTDNIFAKSWA 180
 QY 181 KRKFGFEENKIDRTGTGIPEDFDYID 205
 DB 181 KRKFGFEENKIDRTGTGIPEDFDYID 205

RESULT 3
 ADM83851
 ID ADM83851 standard; protein; 205 AA.
 AC ADM83851;
 XX
 DT 03-JUN-2004 (first entry)
 XX
 DE Human cancer gene 121P1 protein #6.
 XX
 KW Human; cancer gene 121P1; cytostatic; cancer; chromosome 4q; HLA;
 KW human leukocyte antigen; prostate cancer; bladder cancer; kidney cancer;
 KW colon cancer; lung cancer; pancreatic cancer; breast cancer;
 KW cervical cancer; stomach cancer; gene therapy; vaccine.
 OS Homo sapiens.
 XX
 PN US2003223997-A1.
 XX
 PD 04-DEC-2003.
 XX
 PF 28-FEB-2002; 2002US-00087190.
 XX
 PR 08-FEB-2001; 2001US-00779250.
 XX

(CHAL/) CHALLITA-RID P M.
 PA (HUBE/) HUBERT R S.
 PA (RAIT/) RAITANO A B.
 PA (PARI/) PARIS M.
 PA (APAR/) APAR D E H.
 PA (GBW/) GE W.
 PA (JAKO/) JAKOBOWITS A.
 XX

PI Chailita-Eid PM, Hubert RS, Raitano AB, Faris M, Afar DEH, Ge W,
PI Jakobovits A;
XX WPI; 2004-060522/06.
XX
PT New composition comprising a substance that modulates the status of
PT 121PI1 or a molecule that is modulated by 121PI1, useful for detecting,
PT treating or preventing cancer e.g. prostate, bladder, colon, breast or
PT lung cancer.

Example 5; SEQ ID NO 61; 211pp; English.

XX The invention relates to a composition comprising a substance that
XX modulates the status of 121PI1 (a protein encoded by a cancer expressed
XX gene) or a molecule that is modulated by 121PI1 where status of the cell
XX that expresses 121PI1 is modulated. Also included are a pharmaceutical
XX composition comprising the novel composition in a human unit dose form, a
XX recombinant protein comprising an antigen-binding region of a monoclonal
XX antibody, a non-human transgenic animal that produces an antibody, a
XX hybridoma that produces an antibody, a single chain monoclonal antibody
XX that immunospecifically binds to a 121PI1-related protein (comprising
XX the variable domains of the heavy and light chains of a monoclonal
XX antibody), a vector comprising a polynucleotide that encodes a single
XX chain monoclonal antibody, a polynucleotide that encodes an analogue
XX peptide, delivering a cytotoxic agent or a diagnostic agent to a cell
XX that expresses 121PI1, inhibiting growth of cancer cells that expresses
XX 121PI1 (comprising administering to the cells the composition), treating
XX a patient who bears cancer cells that express 121PI1, generating a
XX mammalian immune response directed to 121PI1, inducing an immune
XX response, monitoring 121PI1 gene products in a biological sample from a
XX patient who has or who is suspected of having cancer, monitoring the
XX presence of cancer in an individual and an assay for detecting the
XX presence of a 121PI1-related protein or polynucleotide in a biological
XX sample from a patient who has or who is suspected of having cancer. The
XX composition may comprise a polynucleotide that comprises a 121PI1-
XX related protein coding sequence provided that the coding sequence does
XX not encode the entire amino acid sequence of 121PI1 (ADM83793). The
XX substance also comprises a polynucleotide that encodes at least one
XX peptide given in 16 Tables (given in the specification), the peptides
XX being HLA (human leukocyte antigen)-binding epitopes from 121PI1 or its
XX splice variants. The composition is useful for detecting, treating or
XX preventing cancer, preferably prostate cancer, bladder cancer, kidney
XX cancer, colon cancer, lung cancer, pancreatic cancer, breast cancer,
XX cervical cancer or stomach cancer. The composition can also be used as a
XX vaccine to treat or prevent cancer that expresses or overexpresses
XX 121PI1. The gene for 121PI1 is located on chromosome 4q. The present
XX sequence is a 121PI1 protein (full-length or fragment).

XX Sequence 205 AA;

Query Match 100.0%; Score 1047; DB 8; Length 205;
Beet Local Similarity 100.0%; Pred. No. 1.5e-88;
Matches 205; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSKKKGLSAEKKRTMMEIFSETKQVFOUKDEKTAPEKKGITAMSVKEVLQSLVDGAV 60
DB 1 MSKKKGLSAEKKRTMMEIFSETKQVFOUKDEKTAPEKKGITAMSVKEVLQSLVDGAV 60
QY 61 DCEKIGTSNYVAFPSKALHARKHKLVELESQLSGQFASLOKSIIEFAKIGRCETERR 120
DB 61 DCEKIGTSNYVAFPSKALHARKHKLVELESQLSGQFASLOKSIIEFAKIGRCETERR 120
QY 121 TRLAEELSLRQREOLKAVERKYDCDDQVVEEIRQANKVKAENRNTDNIPIKSWA 180
DB 121 TRLAEELSLRQREOLKAVERKYDCDDQVVEEIRQANKVKAENRNTDNIPIKSWA 180
QY 181 KRKFGFEENKIDRTFGIPEDFDYID 205
DB 181 KRKFGFEENKIDRTFGIPEDFDYID 205

RESULT 4
ADM83810

ID ADM83810 standard; protein, 205 AA.
AC ADM83810;
XX
XX
DT 03-JUN-2004 (first entry)
XX
XX Human cancer gene 121PI1 protein #3.
DE
XX Human; cancer gene 121PI1; cytostatic; cancer; chromosome 4q; HLA;
XX human leukocyte antigen; prostate cancer; bladder cancer; kidney cancer;
XX colon cancer; lung cancer; pancreatic cancer; breast cancer;
XX cervical cancer; stomach cancer; gene therapy; vaccine.
XX
XX Homo sapiens.
OS
XX
XX US2003223997-A1.
XX
XX 04-DEC-2003.
PD
XX
XX 28-FEB-2002; 2002US-00087190.
XX
XX 08-FEB-2001; 2001US-00779250.
PR
XX
XX (CHAL/) CHAILITA-EID P. M.
XX (HUBE/) HUBERT R. S.
XX (RAIT/) RAITANO A. B.
XX (FAR/) FARIS M.
XX (AFAR/) AFAR D E H.
XX (GEW/) GE W.
XX (JAKO/) JAKOBOVITS A.
XX
XX Chailita-Eid PM, Hubert RS, Raitano AB, Faris M, Afar DEH, Ge W,
XX Jakobovits A;
XX WPI; 2004-060522/06.
XX
XX New composition comprising a substance that modulates the status of
XX 121PI1 or a molecule that is modulated by 121PI1, useful for detecting,
XX treating or preventing cancer e.g. prostate, bladder, colon, breast or
XX lung cancer.

PS Disclosure; SEQ ID NO 20; 211pp; English.

XX The invention relates to a composition comprising a substance that
XX modulates the status of 121PI1 (a protein encoded by a cancer expressed
XX gene) or a molecule that is modulated by 121PI1 where status of the cell
XX that expresses 121PI1 is modulated. Also included are a pharmaceutical
XX composition comprising the novel composition in a human unit dose form, a
XX recombinant protein comprising an antigen-binding region of a monoclonal
XX antibody, a non-human transgenic animal that produces an antibody, a
XX hybridoma that produces an antibody, a single chain monoclonal antibody
XX that immunospecifically binds to a 121PI1-related protein (comprising
XX the variable domains of the heavy and light chains of a monoclonal
XX antibody), a vector comprising a polynucleotide that encodes a single
XX chain monoclonal antibody, a polynucleotide that encodes an analogue
XX peptide, delivering a cytotoxic agent or a diagnostic agent to a cell
XX that expresses 121PI1, inhibiting growth of cancer cells that expresses
XX 121PI1 (comprising administering to the cells the composition), treating
XX a patient who bears cancer cells that express 121PI1, generating a
XX mammalian immune response directed to 121PI1, inducing an immune
XX response, monitoring 121PI1 gene products in a biological sample from a
XX patient who has or who is suspected of having cancer, monitoring the
XX presence of cancer in an individual and an assay for detecting the
XX presence of a 121PI1-related protein or polynucleotide in a biological
XX sample from a patient who has or who is suspected of having cancer. The
XX composition may comprise a polynucleotide that comprises a 121PI1-
XX related protein coding sequence provided that the coding sequence does
XX not encode the entire amino acid sequence of 121PI1 (ADM83793). The
XX substance also comprises a polynucleotide that encodes at least one
XX peptide given in 16 Tables (given in the specification), the peptides
XX being HLA (human leukocyte antigen)-binding epitopes from 121PI1 or its
XX splice variants. The composition is useful for detecting, treating or
XX preventing cancer, preferably prostate cancer, bladder cancer, kidney

KW cervical cancer; stomach cancer; gene therapy; vaccine.
 XX Homo sapiens.
 OS
 XX US2003223997-A1.
 PN
 XX 04-DEC-2003.
 PD
 XX 28-FEB-2002; 2002US-00087190.
 PF
 XX 08-FEB-2001; 2001US-00779250.
 PR
 XX (CHAL/) CHALLITA-EID P M.
 PA (HUBE/) HUBERT R S.
 PA (RAIT/) RAITANO A B.
 PA (FARI/) FARIS M.
 PA (AFAR/) AFAR D E H.
 PA (GEWM/) GE W.
 PA (JAKO/) JAKOBOVITS A.
 XX
 PI Challita-Eid PM, Hubert RS, Raitano AB, Faris M, Afar DEH, Ge W;
 PI Jakobovits A;
 DR WPI; 2004-060522/06.
 DR N-PSDB; ADM83792.
 XX
 PT New composition comprising a substance that modulates the status of
 PT 121P1F1 or a molecule that is modulated by 121P1F1, useful for detecting,
 PT treating or preventing cancer e.g. prostate, bladder, colon, breast or
 PT lung cancer.
 PT
 PS Claim 19; SEQ ID NO 3; 211pp; English.
 XX
 CC The invention relates to a composition comprising a substance that
 CC modulates the status of 121P1F1 (a protein encoded by a cancer expressed
 CC gene) or a molecule that is modulated by 121P1F1 where status of the cell
 CC that expresses 121P1F1 is modulated. Also included are a pharmaceutical
 CC composition comprising the novel composition in a human unit dose form, a
 CC recombinant protein comprising an antigen-binding region of a monoclonal
 CC antibody, a non-human transgenic animal that produces an antibody, a
 CC hybridoma that produces an antibody, a single chain monoclonal antibody
 CC that immunospecifically binds to a 121P1F1-related protein (comprising
 CC the variable domains of the heavy and light chains of a monoclonal
 CC antibody), a vector comprising a polynucleotide that encodes a single
 CC chain monoclonal antibody, a polynucleotide that encodes an analogue
 CC peptide, delivering a cytotoxic agent or a diagnostic agent to a cell
 CC that expresses 121P1F1, inhibiting growth of cancer cells that expresses
 CC 121P1F1 (comprising administering to the cells the composition), treating
 CC a patient who bears cancer cells that express 121P1F1, generating a
 CC mammalian immune response directed to 121P1F1, inducing an immune
 CC response, monitoring 121P1F1 gene products in a biological sample from a
 CC patient who has or who is suspected of having cancer, monitoring the
 CC presence of cancer in an individual and an assay for detecting the
 CC presence of a 121P1F1-related protein or polynucleotide in a biological
 CC sample from a patient who has or who is suspected of having cancer. The
 CC composition may comprise a polynucleotide that comprises a 121P1F1-
 CC related protein coding sequence provided that the coding sequence does
 CC not encode the entire amino acid sequence of 121P1F1 (ADM83793). The
 CC substance also comprises a polynucleotide that encodes at least one
 CC peptide given in 16 Tables (given in the specification), the peptides
 CC being HLA (human leukocyte antigen)-binding epitopes from 121P1F1 or its
 CC splice variants. The composition is useful for detecting, treating or
 CC preventing cancer, preferably prostate cancer, bladder cancer, kidney
 CC cancer, colon cancer, lung cancer, pancreatic cancer, breast cancer,
 CC cervical cancer or stomach cancer. The composition can also be used as a
 CC vaccine to treat or prevent cancer that expresses or overexpresses
 CC 121P1F1. The gene for 121P1F1 is located on chromosome 4q. The present
 CC sequence is a 121P1F1 protein (full-length or fragment).
 XX
 SO Sequence 205 AA;
 Query Match 100.0%; Score 1047; DB 8; Length 205;
 Best Local Similarity 100.0%; Pred. No. 1.5e-88;

Matches 205; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSKKGLSAEKRRTMMEIFSETKDVFLQDLKIAPEKKGITAMSVKVLQSLVDGMY 60
 DB 1 MSKKGLSAEKRRTMMEIFSETKDVFLQDLKIAPEKKGITAMSVKVLQSLVDGMY 60
 QY 61 DCRIGTSNYWAPPSKALHARKHLEVLSEQLSGSQHSLQKSIKAKIGRCETER 120
 DB 61 DCRIGTSNYWAPPSKALHARKHLEVLSEQLSGSQHSLQKSIKAKIGRCETER 120
 QY 121 TFLAKELSLRQORQLAEVKKYDCDPQVVEIRQANKVKAANRWTDNIPAIKSWA 180
 DB 121 TFLAKELSLRQORQLAEVKKYDCDPQVVEIRQANKVKAANRWTDNIPAIKSWA 180
 QY 181 KRKFGPEENKIDRTGFIPEDPYID 205
 DB 181 KRKFGPEENKIDRTGFIPEDPYID 205
 RESULT 7
 ID ADM83811
 ID ADM83811 strand; protein; 205 AA.
 XX
 AC ADM83811;
 XX
 DT 03-JUN-2004 (first entry)
 XX
 DE Human cancer gene 121P1F1 protein #4.
 XX
 KW Human; cancer gene 121P1F1; cytostatic; cancer; chromosome 4q; HLA;
 KW human leukocyte antigen; prostate cancer; bladder cancer; kidney cancer;
 KW colon cancer; lung cancer; pancreatic cancer; breast cancer;
 KW cervical cancer; stomach cancer; gene therapy; vaccine.
 XX
 OS Homo sapiens.
 XX
 PN US2003223997-A1.
 XX
 PD 04-DEC-2003.
 XX
 PF 28-FEB-2002; 2002US-00087190.
 XX
 PR 08-FEB-2001; 2001US-00779250.
 XX
 PA (CHAL/) CHALLITA-EID P M.
 PA (HUBE/) HUBERT R S.
 PA (RAIT/) RAITANO A B.
 PA (FARI/) FARIS M.
 PA (AFAR/) AFAR D E H.
 PA (GEWM/) GE W.
 PA (JAKO/) JAKOBOVITS A.
 XX
 PI Challita-Eid PM, Hubert RS, Raitano AB, Faris M, Afar DEH, Ge W;
 PI Jakobovits A;
 DR WPI; 2004-060522/06.
 XX
 PT New composition comprising a substance that modulates the status of
 PT 121P1F1 or a molecule that is modulated by 121P1F1, useful for detecting,
 PT treating or preventing cancer e.g. prostate, bladder, colon, breast or
 PT lung cancer.
 PT
 PS Disclosure; SEQ ID NO 21; 211pp; English.
 XX
 CC The invention relates to a composition comprising a substance that
 CC modulates the status of 121P1F1 (a protein encoded by a cancer expressed
 CC gene) or a molecule that is modulated by 121P1F1 where status of the cell
 CC that expresses 121P1F1 is modulated. Also included are a pharmaceutical
 CC composition comprising the novel composition in a human unit dose form, a
 CC recombinant protein comprising an antigen-binding region of a monoclonal
 CC antibody, a non-human transgenic animal that produces an antibody, a
 CC hybridoma that produces an antibody, a single chain monoclonal antibody
 CC that immunospecifically binds to a 121P1F1-related protein (comprising

the variable domains of the heavy and light chains of a monoclonal antibody, a vector comprising a polynucleotide that encodes a single chain monoclonal antibody, a polynucleotide that encodes a single peptide, delivering a cytotoxic agent or a diagnostic agent to a cell that expresses 121p1, inhibiting growth of cancer cells to a cell 121p1 (comprising administering to the cells the composition), treating a patient who bears cancer cells that express 121p1, generating a response, monitoring 121p1 gene products in a biological sample from a patient who has or who is suspected of having cancer, monitoring the presence of cancer in an individual and an assay for detecting the presence of a 121p1-related protein or polynucleotide in a biological sample from a patient who has or who is suspected of having cancer. The composition may comprise a polynucleotide that encodes a 121p1-related protein coding sequence provided that the coding sequence does not encode the entire amino acid sequence of 121p1 (ADM83793). The substance also comprises a polynucleotide that encodes at least one being HLA (human leukocyte antigen)-binding epitopes from 121p1 or its splice variants. The composition is useful for detecting, treating or preventing cancer, preferably prostate cancer, bladder cancer, kidney cancer, colon cancer, lung cancer, pancreatic cancer, breast cancer, cervical cancer or stomach cancer. The composition can also be used as a vaccine to treat or prevent cancer. The composition can also be used as a sequence is a 121p1 protein (full-length or fragment).

Query Match
Best Local Similarity 100.0%; Score 1047; DB 8; Length 205;
Matches 205; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSKKKGLSAEKKTRMEIFSETKDVOLKLEKIAPEKKGITAMSVKYLQSLVDGAV 60
DB 1 MSKKKGLSAEKKTRMEIFSETKDVOLKLEKIAPEKKGITAMSVKYLQSLVDGAV 60
QY 61 DCEKIGTSNYMAFPKALHARKHLEKLEVSQSGQKASLOKSIKAKIGRCETTER 120
DB 61 DCEKIGTSNYMAFPKALHARKHLEKLEVSQSGQKASLOKSIKAKIGRCETTER 120
QY 121 TRIAKELSLRDOROLKAEVEKYKDCDPVVEIRQANKVAKEANRWTDNIFAIKSWA 180
DB 121 TRIAKELSLRDOROLKAEVEKYKDCDPVVEIRQANKVAKEANRWTDNIFAIKSWA 180
QY 181 KRKFGEEKIKRTTGIGPEDFDYID 205
DB 181 KRKFGEEKIKRTTGIGPEDFDYID 205

RESULT 8
ADM83804
ID ADM83804 standard; protein; 205 AA.
AC ADM83804;
XX
XX
DT 03-JUN-2004 (first entry)
XX
XX
DE Human cancer gene 121p1 protein #2.
XX
XX
KW Human, cancer gene 121p1; cytostatic; cancer; chromosome 4q; HLA;
KW human leukocyte antigen; prostate cancer; bladder cancer; kidney cancer;
KW colon cancer; lung cancer; pancreatic cancer; breast cancer;
XX cervical cancer; stomach cancer; gene therapy; vaccine.
OS Homo sapiens.
XX
XX
PN US200323997-A1.
XX
XX
PD 04-DEC-2003.
XX
XX
PF 28-FEB-2002; 2002US-00087190.

PR 08-FEB-2001; 2001US-00779250.
XX
XX
PA (CHAL/) CHALLITA-RID P M.
PA (HOBE/) HUBERT R S.
PA (RAIT/) RAITANO A B.
PA (FARI/) FARIS M.
PA (AFAR/) AFAR D E H.
PA (GEWM/) GE W.
PA (JAKO/) JAKOBOWITS A.
XX
XX
PI Challita-Rid PM, Hubert RS, Raitano AB, Faris M, Afar DEH, Ge W,
PI Jakobovits A;
XX
XX
DR WPI; 2004-060522/06.
XX
XX
PT New composition comprising a substance that modulates the status of
PT 121p1 or a molecule that is modulated by 121p1, useful for detecting,
PT treating or preventing cancer e.g. prostate, bladder, colon, breast or
XX lung cancer.
XX
XX
PS Disclosure: SEQ ID NO 14; 211p1; English.

The invention relates to a composition comprising a substance that modulates the status of 121p1 (a protein encoded by a cancer expressed gene) or a molecule that is modulated by 121p1 where status of 121p1 recombinant protein comprising the novel composition in a human unit dose form, a antibody, a non-human transgenic animal that produces an antibody, a hybridoma that produces an antibody, a single chain monoclonal antibody that immunospecifically binds to a 121p1-related protein (comprising antibody), a vector comprising a polynucleotide that encodes a single chain monoclonal antibody, a polynucleotide that encodes a single peptide, delivering a cytotoxic agent or a diagnostic agent to a cell that expresses 121p1, inhibiting growth of cancer cells that express 121p1 (comprising administering to the cells the composition), treating a patient who bears cancer cells that express 121p1, generating a response, monitoring 121p1 gene products in a biological sample from a patient who has or who is suspected of having cancer, monitoring the presence of cancer in an individual and an assay for detecting the presence of a 121p1-related protein or polynucleotide in a biological sample from a patient who has or who is suspected of having cancer. The composition may comprise a polynucleotide that encodes a 121p1-related protein coding sequence provided that the coding sequence does not encode the entire amino acid sequence of 121p1 (ADM83793). The substance also comprises a polynucleotide that encodes at least one being HLA (human leukocyte antigen)-binding epitopes from 121p1 or its splice variants. The composition is useful for detecting, treating or preventing cancer, preferably prostate cancer, bladder cancer, kidney cancer, colon cancer, lung cancer, pancreatic cancer, breast cancer, cervical cancer or stomach cancer. The composition can also be used as a vaccine to treat or prevent cancer. The composition can also be used as a sequence is a 121p1 protein (full-length or fragment).

Query Match
Best Local Similarity 100.0%; Score 1047; DB 8; Length 205;
Matches 205; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSKKKGLSAEKKTRMEIFSETKDVOLKLEKIAPEKKGITAMSVKYLQSLVDGAV 60
DB 1 MSKKKGLSAEKKTRMEIFSETKDVOLKLEKIAPEKKGITAMSVKYLQSLVDGAV 60
QY 61 DCEKIGTSNYMAFPKALHARKHLEKLEVSQSGQKASLOKSIKAKIGRCETTER 120
DB 61 DCEKIGTSNYMAFPKALHARKHLEKLEVSQSGQKASLOKSIKAKIGRCETTER 120
QY 121 TRIAKELSLRDOROLKAEVEKYKDCDPVVEIRQANKVAKEANRWTDNIFAIKSWA 180

DB 121 TRLAKELSLRQREQLKAEVEKYDCDPQVVEIRQANKVAKKANRWTDNI FALKSWA 180
 QY 181 KRKFGFEENKIDRTFGIPEDFDYID 205
 DB 181 KRKFGFEENKIDRTFGIPEDFDYID 205

RESULT 9
 ABP75541
 ID ABP75541 standard; protein; 219 AA.
 AC ABP75541;
 DT 10-FEB-2003 (first entry)
 XX
 DE Human secretory polypeptide SPTM SEQ ID NO 725.
 XX
 KW Human; SPTM; autoimmune disorder; inflammatory disorder; AIDS; anaemia;
 KW asthma; Crohn's disease; neurological disorder; epilepsy; cancer;
 KW Huntington's disease; Alzheimer's disease; Creutzfeldt-Jakob disease;
 KW multiple sclerosis; Parkinson's disease; cell proliferative disorder;
 KW anti-inflammatory; immunosuppressive; neuroprotective; nocrotopic;
 KW neuroleptic; anticonvulsant; cyostatic; antiparkinsonian; anxiolytic;
 KW antipsoriatic; antianaemic; anti-HIV; human immunodeficiency virus;
 KW secretory polynucleotide; secretory protein.
 XX
 OS Homo sapiens.
 XX
 PN WO200283876-A2.
 XX
 PD 24-OCT-2002.
 XX
 PF 27-MAR-2002; 2002WO-US009921.
 XX
 PR 29-MAR-2001; 2001US-0280067P.
 PR 29-MAR-2001; 2001US-0280068P.
 PR 16-MAY-2001; 2001US-0291280P.
 PR 17-MAY-2001; 2001US-0291829P.
 PR 17-MAY-2001; 2001US-0291849P.
 PR 19-JUN-2001; 2001US-0299428P.
 PR 20-JUN-2001; 2001US-0299776P.
 PR 20-JUN-2001; 2001US-0300001P.
 XX
 PA (INCY-) INCYTE GENOMICS INC.
 XX
 PI Daffo A, Jones AL, Tran AB, Dahl CR, Gietzen D, Chinn J;
 PI Dufour GE, Hillman JL, Yu JY, Tuason O, Yap PE, Amshey SR;
 PI Daughtery SC, Dam TC, Liu TF, Nguyen DA, Kleefeld Y, Gerstlin EH;
 PI Peralta CH, David MH, Lewis SA, Chen AJ, Panzer SR, Harris B;
 PI Flores V, Marwaha R, Lo A, Lan RY, Urashka ME;
 XX
 DR WPI; 2003-075543/07.
 DR N-PSDB; ABZ35987.
 XX
 PT New human secretory proteins and polynucleotides, useful for diagnosing,
 PT treating or preventing autoimmune/inflammatory disorders (e.g. AIDS),
 PT neurological disorders (e.g. Alzheimer's), or cell proliferations or
 PT cancers.
 XX
 PS Claim 27; SEQ ID NO 725; 458bp + Sequence Listing; English.
 XX
 CC The invention relates to a secretory polynucleotide (designated spm)
 CC comprising any of 567 polynucleotide sequences (ABZ35837-ABZ36403), a
 CC naturally occurring polynucleotide sequence at least 90 % identical to
 CC the polynucleotide sequence, a polynucleotide complementary to them or an
 CC RNA equivalent of them. The polypeptide or polynucleotide are useful for
 CC treating, preventing or diagnosing a disease or condition associated with
 CC the expression of functional SPTM. These are particularly useful for
 CC diagnosing, treating or preventing autoimmune/inflammatory disorders
 CC (e.g. acquired immunodeficiency syndrome, anaemia, asthma or Crohn's
 CC disease), neurological disorders (e.g. epilepsy, Huntington's disease,
 CC dementia, stroke, Alzheimer's disease, Creutzfeldt-Jakob disease,

CC multiple sclerosis, cerebral palsy, Parkinson's disease, anxiety,
 CC schizophrenia or amnesia), or cell proliferative disorders (e.g.
 CC psoriasis, polycythemia vera, or cancers including adenocarcinoma,
 CC leukaemia, lymphoma, melanoma, myeloma, sarcoma or cancers of the brain,
 CC breast, cervix or prostate). The present sequence is one of the SPTM
 CC proteins of the invention (ABP75384-ABP75962). Note: The sequence data
 CC for this patent did not form part of the printed specification, but was
 CC obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 219 AA;
 Query Match 100.0%; Score 1047; DB 6; Length 219;
 Best Local Similarity 100.0%; Pred. No. 1.7e-88;
 Matches 205; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSKKKGLSNEEKRTMMEIFSETKVPQKDKLEKAPKPKGTITANSYKVELSLVDGKV 60
 DB 15 MSKKKGLSNEEKRTMMEIFSETKVPQKDKLEKAPKPKGTITANSYKVELSLVDGKV 74
 QY 61 DCRIGTSNYWAFPSKALHARKHLEVLSEGLSGSQKASLQKSIKAKIGRCETTER 120
 DB 75 DCRIGTSNYWAFPSKALHARKHLEVLSEGLSGSQKASLQKSIKAKIGRCETTER 134
 QY 121 TRLAKELSLRQREQLKAEVEKYDCDPQVVEIRQANKVAKKANRWTDNI FALKSWA 180
 DB 135 TRLAKELSLRQREQLKAEVEKYDCDPQVVEIRQANKVAKKANRWTDNI FALKSWA 194

QY 181 KRKFGFEENKIDRTFGIPEDFDYID 205
 DB 195 KRKFGFEENKIDRTFGIPEDFDYID 219

RESULT 10
 ADM83834
 ID ADM83834 standard; protein; 206 AA.
 XX
 AC ADM83834;
 XX
 DT 03-JUN-2004 (first entry)
 XX
 DE Human cancer gene 121P1F1 variant protein #1.
 XX
 DE Human; cancer gene 121P1F1; cyostatic; cancer; chromosome 4q; HLA;
 KW human leukocyte antigen; prostate cancer; bladder cancer; kidney cancer;
 KW colon cancer; lung cancer; pancreatic cancer; breast cancer;
 KW cervical cancer; stomach cancer; gene therapy; vaccine.
 XX
 OS Homo sapiens.
 XX
 PN US2003223997-A1.
 XX
 PD 04-DEC-2003.
 XX
 PF 28-FEB-2002; 2002US-00087190.
 XX
 PR 08-FEB-2001; 2001US-00779250.
 XX
 PA (CHAL/) CHALLITA-EID P M.
 PA (HUBE/) HUBERT R S.
 PA (RAIT/) RAITANO A B.
 PA (FARI/) FARIS M.
 PA (AFAR/) AFAR D E H.
 PA (GEWW/) GE W.
 PA (JAKO/) JAKOBOVITS A.
 XX
 PI Chailita-Eid PM, Hubert RS, Raitano AB, Faris M, Afar DEH, Ge W;
 PI Jakobovits A;
 XX
 DR WPI; 2004-060522/06.
 XX
 PT New composition comprising a substance that modulates the status of
 PT 121P1F1 or a molecule that is modulated by 121P1F1, useful for detecting,

PT creating or preventing cancer e.g. prostate, bladder, colon, breast or
 PT lung cancer.
 XX

PS Example 5; SEQ ID NO 44; 211bp; English.
 XX

CC The invention relates to a composition comprising a substance that
 CC modulates the status of 121p1f1 (a protein encoded by a cancer gene)
 CC (gene) or a molecule that is modulated by 121p1f1 where status of the cell
 CC composition comprising 121p1f1 is modulated. Also included are a pharmaceutical
 CC recombinant protein comprising an antigen-binding region of a monoclonal
 CC antibody, a non-human transgenic animal that produces an antibody, a
 CC hybridoma that produces an antibody, a single chain monoclonal antibody
 CC that immunospecifically binds to a 121p1f1-related protein (comprising
 CC chain monoclonal antibody, a polynucleotide that encodes a single
 CC peptide, delivering a cytotoxic agent or a diagnostic agent to a cell
 CC 121p1f1 (comprising administering to the cells the composition), treating
 CC a patient who bears cancer cells that express 121p1f1, generating a
 CC mammalian immune response directed to 121p1f1, inducing an immune
 CC response, monitoring 121p1f1 gene products in a biological sample from a
 CC patient who has or who is suspected of having cancer, monitoring the
 CC presence of cancer in an individual and an assay for detecting the
 CC sample from a patient who has or who is suspected of having cancer. The
 CC composition may comprise a polynucleotide that comprises a 121p1f1-
 CC related protein coding sequence provided that the coding sequence does
 CC not encode the entire amino acid sequence of 121p1f1 (ADN63793). The
 CC substance also comprises a polynucleotide that encodes at least one
 CC peptide given in 16 Tables (given in the specification), the peptides
 CC being HLA (human leukocyte antigen)-binding epitopes from 121p1f1 or its
 CC splice variants. The composition is useful for detecting, treating or
 CC preventing cancer, preferably prostate cancer, bladder cancer, kidney
 CC cancer, colon cancer, lung cancer, pancreatic cancer, breast cancer,
 CC cervical cancer or stomach cancer. The composition can also be used as a
 CC vaccine to treat or prevent cancer that expresses or overexpresses
 CC 121p1f1. The gene for 121p1f1 is located on chromosome 4q. The present
 CC sequence is a 121p1f1 protein (full-length or fragment).
 XX
 SQ Sequence 206 AA;

Query Match 99.0%; Score 1036.5; DB 8; Length 206;
 Best Local Similarity 99.5%; Pred. No. 1.4e-87;
 Matches 205; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MSKKKGLSAEKKRTMWEISETYDVFQLEKIAPEKXGTTANSVYVQLQSLVDDGMV 60
 DB 1 MSKKKGLSAEKKRTMWEISETYDVFQLEKIAPEKXGTTANSVYVQLQSLVDDGMV 60
 QY 61 DCEERTGTSNYWAPSPALHARKKLEVES-QLSEGGOKIASLQKSTIEKAKICRCTEE 119
 DB 61 DCEERTGTSNYWAPSPALHARKKLEVES-QLSEGGOKIASLQKSTIEKAKICRCTEE 119
 QY 120 RTRIAKELSSLRQRFQDLKAEVEKYYCDPQVEIRIQAANKVAEANKRNTDVIPIKSW 179
 DB 120 RTRIAKELSSLRQRFQDLKAEVEKYYCDPQVEIRIQAANKVAEANKRNTDVIPIKSW 179
 QY 121 RTRIAKELSSLRQRFQDLKAEVEKYYCDPQVEIRIQAANKVAEANKRNTDVIPIKSW 180
 DB 121 RTRIAKELSSLRQRFQDLKAEVEKYYCDPQVEIRIQAANKVAEANKRNTDVIPIKSW 180
 QY 180 AKRFGGEENKIDRTFGIPEDFDYID 205
 DB 180 AKRFGGEENKIDRTFGIPEDFDYID 205
 QY 181 AKRFGGEENKIDRTFGIPEDFDYID 206
 DB 181 AKRFGGEENKIDRTFGIPEDFDYID 206

RESULT 11
 ADN63835
 ID ADN63835 standard; protein, 206 AA.
 XX
 AC ADN63835;
 XX
 DT 03-JUN-2004 (first entry)
 XX
 DE Human cancer gene 121p1f1 variant protein #2.

XX
 KW Human, cancer gene 121p1f1, cytostatic; cancer; chromosome 4q; HLA;
 KW human leukocyte antigen; prostate cancer; bladder cancer; kidney cancer;
 KW cervical cancer; lung cancer; pancreatic cancer; breast cancer;
 XX
 OS Homo sapiens.
 XX
 PN US2003223997-A1.
 XX
 PD 04-DEC-2003.
 XX
 PF 28-FEB-2002; 2002US-00087190.
 XX
 PR 08-FEB-2001; 2001US-00779250.
 XX
 PA (CHAL/) CHALITA-BID P. M.
 PA (HUBE/) HUBERT R. S.
 PA (RAIT/) RAITANO A. B.
 PA (FART/) FARTIS M.
 PA (APAR/) AFAR D E H.
 PA (GEMW/) GE W.
 PA (JAKO/) JAKOBOVITS A.
 XX
 PI Chailita-Bid PM, Hubert RS, Raitano AB, Fartis M, Afar DEH, Ge W,
 PI Jakobovits A;
 XX
 DR WPI, 2004-060522/06.
 XX
 PT New composition comprising a substance that modulates the status of
 PT 121p1f1 or a molecule that is modulated by 121p1f1, useful for detecting,
 PT treating or preventing cancer e.g. prostate, bladder, colon, breast or
 PT lung cancer.
 XX
 XX Example 5; SEQ ID NO 45; 211bp; English.
 CC The invention relates to a composition comprising a substance that
 CC modulates the status of 121p1f1 (a protein encoded by a cancer gene)
 CC (gene) or a molecule that is modulated by 121p1f1 where status of the cell
 CC composition comprising 121p1f1 is modulated. Also included are a pharmaceutical
 CC recombinant protein comprising an antigen-binding region of a monoclonal
 CC antibody, a non-human transgenic animal that produces an antibody, a
 CC hybridoma that produces an antibody, a single chain monoclonal antibody
 CC that immunospecifically binds to a 121p1f1-related protein (comprising
 CC chain monoclonal antibody, a polynucleotide that encodes a single
 CC peptide, delivering a cytotoxic agent or a diagnostic agent to a cell
 CC 121p1f1 (comprising administering to the cells the composition), treating
 CC a patient who bears cancer cells that express 121p1f1, generating a
 CC mammalian immune response directed to 121p1f1, inducing an immune
 CC response, monitoring 121p1f1 gene products in a biological sample from a
 CC patient who has or who is suspected of having cancer, monitoring the
 CC presence of cancer in an individual and an assay for detecting the
 CC sample from a patient who has or who is suspected of having cancer. The
 CC composition may comprise a polynucleotide that comprises a 121p1f1-
 CC related protein coding sequence provided that the coding sequence does
 CC not encode the entire amino acid sequence of 121p1f1 (ADN63793). The
 CC substance also comprises a polynucleotide that encodes a single
 CC peptide given in 16 Tables (given in the specification), the peptides
 CC being HLA (human leukocyte antigen)-binding epitopes from 121p1f1 or its
 CC splice variants. The composition is useful for detecting, treating or
 CC preventing cancer, preferably prostate cancer, bladder cancer, kidney
 CC cancer, colon cancer, lung cancer, pancreatic cancer, breast cancer,
 CC cervical cancer or stomach cancer. The composition can also be used as a
 CC vaccine to treat or prevent cancer that expresses or overexpresses
 CC 121p1f1. The gene for 121p1f1 is located on chromosome 4q. The present
 CC sequence is a 121p1f1 protein (full-length or fragment).
 XX
 SQ Sequence 206 AA;

Query Match 99.0%; Score 1036.5; DB 8; Length 206;
 Best Local Similarity 99.5%; Pred. No. 1.4e-87;
 Matches 205; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MSKKGLSAEKRTRMMEIFSETKDVFOJLKDLEKIAPKKEGKTAMSVKEVLSLVDDGMV 60
 DB 1 MSKKGLSAEKRTRMMEIFSETKDVFOJLKDLEKIAPKKEGKTAMSVKEVLSLVDDGMV 60
 QY 61 DCEKGTGNTYVAFPSKALHARKHLEVEESQ-LSRGSQKHAISLOKSIKARTGCTEE 119
 DB 61 DCEKGTGNTYVAFPSKALHARKHLEVEESQ-LSRGSQKHAISLOKSIKARTGCTEE 120
 QY 120 RTRLAKELSLRDQREQLKAEVEKYKDCDPQVVEIRQANKYAKKANRMTDNIFAISK 179
 DB 121 RTRLAKELSLRDQREQLKAEVEKYKDCDPQVVEIRQANKYAKKANRMTDNIFAISK 180
 QY 180 AKRKGFEENKIDRTFGIPEDFDYID 205
 DB 181 AKRKGFEENKIDRTFGIPEDFDYID 206

RESULT 12
 ADM83814
 ID ADM83814 standard; protein; 198 AA.
 AC ADM83814;
 DT 03-JUN-2004 (first entry)
 XX Human cancer gene 121P1F1 protein fragment.
 DE XX
 KW Human; cancer gene 121P1F1; cytostatic; cancer; chromosome 4q; HLA;
 KM human leukocyte antigen; prostate cancer; bladder cancer; kidney cancer;
 KW colon cancer; lung cancer; pancreatic cancer; breast cancer;
 KM cervical cancer; stomach cancer; gene therapy; vaccine.
 XX Homo sapiens.
 OS US2003223997-A1.
 PN 04-DEC-2003.
 PD 28-FEB-2002; 2002US-00087190.
 PF 08-FEB-2001; 2001US-00779250.
 PR (CHAL/) CHALLITA-EID P M.
 XX (HUBE/) HUBERT R S.
 PA (RAIT/) RAITANO A B.
 PA (FARI/) FARIS M.
 PA (AFAR/) AFAR D E H.
 PA (GEW/) GE W.
 PA (JAKO/) JAKOBOVITS A.
 XX
 PI Chailita-Eid PM, Hubert RS, Raitano AB, Faris M, Afar DEH, Ge W;
 PI Jakobovits A;
 DR WPI; 2004-060522/06.
 XX
 PT New composition comprising a substance that modulates the status of
 PT 121P1F1 or a molecule that is modulated by 121P1F1, useful for detecting,
 PT treating or preventing cancer e.g. prostate, bladder, colon, breast or
 PT lung cancer.
 XX
 PS Example 2; SEQ ID NO 24; 211pp; English.
 XX
 CC The invention relates to a composition comprising a substance that
 CC modulates the status of 121P1F1 (a protein encoded by a cancer expressed
 CC gene) or a molecule that is modulated by 121P1F1 where status of the cell
 CC that expresses 121P1F1 is modulated. Also included are a pharmaceutical
 CC composition comprising the novel composition in a human unit dose form, a
 CC recombinant protein comprising an antigen-binding region of a monoclonal

CC antibody, a non-human transgenic animal that produces an antibody, a
 CC hybridoma that produces an antibody, a single chain monoclonal antibody
 CC that immunospecifically binds to a 121P1F1-related protein (comprising
 CC the variable domains of the heavy and light chains of a monoclonal
 CC antibody), a vector comprising a polynucleotide that encodes a single
 CC chain monoclonal antibody, a polynucleotide that encodes an analogue
 CC peptide, delivering a cytotoxic agent or a diagnostic agent to a cell
 CC that expresses 121P1F1, inhibiting growth of cancer cells that expresses
 CC 121P1F1 (comprising administering to the cells the composition), treating
 CC a patient who bears cancer cells that express 121P1F1, generating a
 CC mammalian immune response directed to 121P1F1, inducing an immune
 CC response, monitoring 121P1F1 gene products in a biological sample from a
 CC patient who has or who is suspected of having cancer, monitoring the
 CC presence of cancer in an individual and an assay for detecting the
 CC presence of a 121P1F1-related protein or polynucleotide in a biological
 CC sample from a patient who has or who is suspected of having cancer. The
 CC composition may comprise a polynucleotide that comprises a 121P1F1-
 CC related protein coding sequence provided that the coding sequence does
 CC not encode the entire amino acid sequence of 121P1F1 (ADM83793). The
 CC substance also comprises a polynucleotide that encodes at least one
 CC peptide given in 16 Tables (given in the specification), the peptides
 CC being HLA (human leukocyte antigen)-binding epitopes from 121P1F1 or its
 CC splice variants. The composition is useful for detecting, treating or
 CC preventing cancer, preferably prostate cancer, bladder cancer, kidney
 CC cancer, colon cancer, lung cancer, pancreatic cancer, breast cancer,
 CC cervical cancer or stomach cancer. The composition can also be used as a
 CC vaccine to treat or prevent cancer that expresses or overexpresses
 CC 121P1F1. The gene for 121P1F1 is located on chromosome 4q. The present
 CC sequence is a 121P1F1 protein (full-length or fragment).
 XX
 SQ Sequence 198 AA;

Query Match 96.6%; Score 1011; DB 8; Length 198;
 Best Local Similarity 100.0%; Pred. No. 3.1e-85;
 Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KGLSAEKRTRMMEIFSETKDVFOJLKDLEKIAPKKEGKTAMSVKEVLSLVDDGMVDCR 64
 DB 1 KGLSAEKRTRMMEIFSETKDVFOJLKDLEKIAPKKEGKTAMSVKEVLSLVDDGMVDCR 60
 QY 65 IGTSNYYVAFPSKALHARKHLEVEESQ-LSRGSQKHAISLOKSIKARTGCTEERTLA 124
 DB 61 IGTSNYYVAFPSKALHARKHLEVEESQ-LSRGSQKHAISLOKSIKARTGCTEERTLA 120
 QY 125 KELSLRDQREQLKAEVEKYKDCDPQVVEIRQANKYAKKANRMTDNIFAISKAKRF 184
 DB 121 KELSLRDQREQLKAEVEKYKDCDPQVVEIRQANKYAKKANRMTDNIFAISKAKRF 180
 QY 185 GFENKIDRTFGIPEDFD 202
 DB 181 GFENKIDRTFGIPEDFD 198

RESULT 13
 AAM40043
 ID AAM40043 standard; protein; 190 AA.
 AC AAM40043;
 DT 22-OCT-2001 (first entry)
 XX Human polypeptide SEQ ID NO 3188.
 DE XX
 KW Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
 KW peripheral nervous system; neuropathy; central nervous system; CNS;
 KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
 KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
 KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
 XX leukaemia.
 OS Homo sapiens.
 XX WO200153312-A1.
 PN

XX 26-JUL-2001.
 XX 26-DEC-2000; 2000MO-US034263.
 PF 23-DEC-1999; 99US-00471275.
 PR 21-JAN-2000; 2000US-00488725.
 PR 25-APR-2000; 2000US-00552317.
 PR 20-JUN-2000; 2000US-00552317.
 PR 19-JUL-2000; 2000US-00598042.
 PR 03-AUG-2000; 2000US-00620312.
 PR 14-SEP-2000; 2000US-00653450.
 PR 19-OCT-2000; 2000US-00662191.
 PR 29-NOV-2000; 2000US-00693036.
 XX (HYSE-) HYSEQ INC.
 PA Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
 PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;
 PR Zhou P, Goodrich R, Drmanac RT;
 DR WPI; 2001-442253/47.
 N-PSDB; AA159199.
 XX Novel nucleic acids and polypeptides, useful for treating disorders such
 PT as central nervous system injuries.
 XX Example 4; SEQ ID NO 3188; 10078bp; English.
 PS The invention relates to human nucleic acids (AA157798-AA161369) and the
 CC encoded polypeptides (AA158642-AA162213) with neurotrophic,
 CC immunosuppressant and cytostatic activity. The polynucleotides are useful
 CC in gene therapy. A composition containing a polypeptide or polynucleotide
 CC of the invention may be used to treat diseases of the peripheral nervous
 CC system, such as peripheral nervous injuries, peripheral neuropathy and
 CC localized neuropathies and central nervous system diseases, such as
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
 CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
 CC activation of the activities such as: immune system suppression,
 CC inhibition of inhibitory activity, chemotactic/chemokinetic activity, haemostatic
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
 CC assays for receptor activity, arthritis and inflammation, leukemias and
 CC C.N.S disorders. Note: The sequence data for this patent did not form
 CC part of the printed specification
 XX Sequence 190 AA;
 SQ
 Query Match 93.1%; Score 975; DB 4; Length 190;
 Best Local Similarity 100.0%; Pred. No. 6.3e-82;
 Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 16 MMEIFSEKDVFOLEKLEKIAPEKIGITAMSVKYLQSLVDDGWDGVCERTIGTSYVWAPF 75
 DB 1 MMEIFSEKDVFOLEKLEKIAPEKIGITAMSVKYLQSLVDDGWDGVCERTIGTSYVWAPF 75
 QY 76 SKALHARKHLEVLSEQLSEGSOKHSLQKSTIEKAKIGRCETERTRLAKELSLDDQRE 135
 DB 61 SKALHARKHLEVLSEQLSEGSOKHSLQKSTIEKAKIGRCETERTRLAKELSLDDQRE 135
 QY 136 QLAFAVEKVKDDCPQVEIRQANKVAKAANRWTDNIFAISKMARCKGFENKIDRTF 195
 DB 121 QLAFAVEKVKDDCPQVEIRQANKVAKAANRWTDNIFAISKMARCKGFENKIDRTF 195
 QY 196 GIPEDPDYID 205
 DB 181 GIPEDPDYID 190

XX 29-JAN-2004 (first entry)
 DT 121PIF1 variant 4 protein.
 XX 121PIF1, 121PIF1 modulation; human; chromosome 4q; cytostatic;
 KW gene therapy; vaccine; cancer; immune response; immunisation.
 XX Synthetic.
 OS Homo sapiens.
 XX WO200295009-A2.
 PN 28-NOV-2002.
 PD 28-FEB-2002; 2002WO-US006242.
 PF 05-MAR-2001; 2001US-00799250.
 PR (AGEN-) AGENSYS INC.
 PA Challita-Eid PM, Hubert RS, Raitano AB, Faris M, Afar DH, Ge W;
 PI Jakobovits AJ;
 DR WPI; 2003-156757/15.
 N-PSDB; ADD84546.
 XX Composition comprising a substance that modulates the status of 121PIF1,
 PT useful in diagnosing, preventing, prognosticating or treating patients
 PT with cancer that expresses 121PIF1, such as breast, colon, ovarian or
 PS lung cancer.
 Claim 19; Fig 2F; 285bp; English.
 CC The present invention describes a composition (I) comprising a substance
 CC that modulates the status of 121PIF1 (gene and encoded protein), or a
 CC molecule that is modulated by 121PIF1, where the status of a cell that
 CC expresses 121PIF1 is modulated. The human 121PIF1 gene maps to chromosome
 CC 4q. (I) has cytostatic activity, and can be used in gene therapy, and in
 CC prognosticating or treating patients with cancer that expresses 121PIF1,
 CC such as breast, colon, ovarian or lung cancer. The 121PIF1 gene or its
 CC fragment can be used to elicit a humoral or cellular immune response.
 CC 121PIF1 antibodies can be used in active or passive immunisation. 121PIF1
 CC polynucleotides are useful as probes and primers for the amplification or
 CC expression of 121PIF1 genes, as coding sequences for directing the
 CC inhibiting the expression of 121PIF1 genes. The present sequence is used
 CC in the exemplification of the present invention.
 XX Sequence 190 AA;
 SQ
 Query Match 93.1%; Score 975; DB 7; Length 190;
 Best Local Similarity 100.0%; Pred. No. 6.3e-82;
 Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 16 MMEIFSEKDVFOLEKLEKIAPEKIGITAMSVKYLQSLVDDGWDGVCERTIGTSYVWAPF 75
 DB 1 MMEIFSEKDVFOLEKLEKIAPEKIGITAMSVKYLQSLVDDGWDGVCERTIGTSYVWAPF 75
 QY 76 SKALHARKHLEVLSEQLSEGSOKHSLQKSTIEKAKIGRCETERTRLAKELSLDDQRE 135
 DB 61 SKALHARKHLEVLSEQLSEGSOKHSLQKSTIEKAKIGRCETERTRLAKELSLDDQRE 135
 QY 136 QLAFAVEKVKDDCPQVEIRQANKVAKAANRWTDNIFAISKMARCKGFENKIDRTF 195
 DB 121 QLAFAVEKVKDDCPQVEIRQANKVAKAANRWTDNIFAISKMARCKGFENKIDRTF 195
 QY 196 GIPEDPDYID 205
 DB 181 GIPEDPDYID 190

RESULT 14
 ADD84547
 ID ADD84547 standard; protein; 190 AA.
 XX
 AC ADD84547;

RESULT 15
ADM83857
ADM83857 standard; protein; 190 AA.
XX
AC ADM83857;
XX
DT 03-JUN-2004 (first entry)
XX
DE Human cancer gene 121P1F1 protein 16-205.
XX
KM Human; cancer gene 121P1F1; cytostatic; cancer; chromosome 4q; HLA;
KM human leukocyte antigen; prostate cancer; bladder cancer; kidney cancer;
KM colon cancer; lung cancer; pancreatic cancer; breast cancer;
KM cervical cancer; stomach cancer; gene therapy; vaccine.
XX
OS Homo sapiens.
XX
PN US2003223997-A1.
XX
PD 04-DEC-2003.
XX
PF 28-FEB-2002; 2002US-00087190.
PR 08-FEB-2001; 2001US-0079250.
XX
PA (CHAL/) CHALLITA-ElD P M.
PA (HUBE/) HUBERT R S.
PA (RAIT/) RAITANO A B.
PA (FARI/) FARIS M.
PA (AFAR/) AFAR D E H.
PA (GEWA/) GE W.
PA (JAKO/) JAKOBOVITS A.
XX
PI Challaite-ElD PM, Hubert RS, Raitano AB, Faris M, Afar DEH, Ge W;
PI Jakobovits A;
XX
DR WPI; 2004-060522/06.
XX
PT New composition comprising a substance that modulates the status of
PT 121P1F1 or a molecule that is modulated by 121P1F1, useful for detecting,
PT treating or preventing cancer e.g. prostate, bladder, colon, breast or
PT lung cancer.
XX
PS Example 5; SEQ ID NO 67; 211pp; English.
XX
CC The invention relates to a composition comprising a substance that
CC modulates the status of 121P1F1 (a protein encoded by a cancer expressed
CC gene) or a molecule that is modulated by 121P1F1 where status of the cell
CC that expresses 121P1F1 is modulated. Also included are a pharmaceutical
CC composition comprising the novel composition in a human unit dose form, a
CC recombinant protein comprising an antigen-binding region of a monoclonal
CC antibody, a non-human transgenic animal that produces an antibody, a
CC hybridoma that produces an antibody, a single chain monoclonal antibody
CC that immunospecifically binds to a 121P1F1-related protein (comprising
CC the variable domains of the heavy and light chains of a monoclonal
CC antibody), a vector comprising a polynucleotide that encodes a single
CC chain monoclonal antibody, a polynucleotide that encodes an analogue
CC peptide, delivering a cytotoxic agent or a diagnostic agent to a cell
CC that expresses 121P1F1, inhibiting growth of cancer cells that expresses
CC 121P1F1 (comprising administering to the cells the composition), treating
CC a patient who bears cancer cells that express 121P1F1, generating a
CC mammalian immune response directed to 121P1F1, inducing an immune
CC response, monitoring 121P1F1 gene products in a biological sample from a
CC patient who has or who is suspected of having cancer, monitoring the
CC presence of cancer in an individual and an assay for detecting the
CC presence of a 121P1F1-related protein or polynucleotide in a biological
CC sample from a patient who has or who is suspected of having cancer. The
CC composition may comprise a polynucleotide that comprises a 121P1F1-
CC related protein coding sequence provided that the coding sequence does
CC not encode the entire amino acid sequence of 121P1F1 (ADM83793). The
CC substance also comprises a polynucleotide that encodes at least one
CC peptide given in 16 tables (given in the specification), the peptides
CC being HLA (human leukocyte antigen)-binding epitopes from 121P1F1 or its

CC splice variants. The composition is useful for detecting, treating or
CC preventing cancer, preferably prostate cancer, bladder cancer, kidney
CC cancer, colon cancer, lung cancer, pancreatic cancer, breast cancer,
CC cervical cancer or stomach cancer. The composition can also be used as a
CC vaccine to treat or prevent cancer that expresses or overexpresses
CC 121P1F1. The gene for 121P1F1 is located on chromosome 4q. The present
CC sequence is a 121P1F1 protein (full-length or fragment).
XX
SQ Sequence 190 AA;
Query Match 93.1%; Score 975; DB 8; Length 190;
Best Local Similarity 100.0%; Fred. No. 6.3e-82;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 16 MMEIFSETKDVFPQLDKLEKIAPEKEGITPMASYKEVLOSIVDDGMVDCERIGTSNYMARP 75
DB 1 MMEIFSETKDVFPQLDKLEKIAPEKEGITPMASYKEVLOSIVDDGMVDCERIGTSNYMARP 60
QY 76 SKALHARKKLELVLESQSEGSQKXASLOKSIKAKIGRCETEERTRLAKELSLRDQRE 135
DB 61 SKALHARKKLELVLESQSEGSQKXASLOKSIKAKIGRCETEERTRLAKELSLRDQRE 120
QY 136 QLKAEVEKKDCDPQVEVERIRQANKVAKAARWTDNIFAIKSMARKKGFENKIDRF 195
DB 121 QLKAEVEKKDCDPQVEVERIRQANKVAKAARWTDNIFAIKSMARKKGFENKIDRF 180
QY 196 GIPEDDPYID 205
DB 181 GIPEDDPYID 190

Search completed: March 23, 2005, 19:14:48
Job time : 171 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 23, 2005, 19:09:32 ; Search time 43 Seconds
(without alignments)
355.885 Million cell updates/sec

Title: US-10-087-190-3

Perfect score: 1047
Sequence: 1 MSKKGSLAEKRTMMEIF.....FEENKIDRTFGIPEDFYID 205

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Issued_Patents_AA:*

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- 2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*
- 3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep:*
- 4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep:*
- 5: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep:*
- 6: /cgn2_6/ptodata/1/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	593.5	56.7	127	US-09-621-976-4959	Sequence 4959, Ap
2	191.5	18.3	260	US-09-248-796A-14485	Sequence 14485, A
3	134.5	12.8	1270	US-09-538-092-1321	Sequence 1321, Ap
4	117	11.2	976	US-09-104-324B-4	Sequence 4, Appl
5	117	11.2	976	US-09-538-092-1339	Sequence 1339, Ap
6	114	10.9	284	US-09-914-259-55	Sequence 55, Appl
7	113.5	10.8	284	US-09-914-259-62	Sequence 62, Appl
8	112.5	10.7	630	US-09-248-796A-20275	Sequence 20275, A
9	112	10.7	284	US-09-914-259-43	Sequence 43, Appl
10	111	10.6	1937	US-09-538-092-918	Sequence 918, Appl
11	110	10.5	284	US-09-914-259-46	Sequence 46, Appl
12	110	10.5	284	US-09-914-259-49	Sequence 49, Appl
13	109.5	10.5	170	US-09-438-185A-708	Sequence 708, Appl
14	109	10.4	284	US-09-914-259-51	Sequence 51, Appl
15	108	10.3	817	US-09-248-796A-20276	Sequence 20276, A
16	107	10.2	281	US-09-914-259-63	Sequence 63, Appl
17	107	10.2	284	US-09-167-206-10	Sequence 10, Appl
18	107	10.2	284	US-09-914-259-40	Sequence 40, Appl
19	107	10.2	284	US-09-914-259-48	Sequence 48, Appl
20	107	10.2	284	US-09-914-259-50	Sequence 50, Appl
21	106.5	10.2	284	US-09-914-259-41	Sequence 41, Appl
22	106	10.1	534	US-09-103-664A-2	Sequence 2, Appl
23	106	10.1	1786	US-08-973-462-8	Sequence 16, Appl
24	105.5	10.1	224	US-08-272-255-16	Sequence 16, Appl
25	105.5	10.1	224	PCT-US95-08565-16	Sequence 34, Appl
26	105.5	10.1	245	US-10-164-595-34	Sequence 65, Appl
27	105	10.0	245	US-09-914-259-65	

28	105	10.0	251	4	US-09-914-259-64	Sequence 64, Appl
29	105	10.0	284	4	US-09-914-259-60	Sequence 60, Appl
30	104	9.9	1939	4	US-09-538-092-915	Sequence 915, Appl
31	104	9.9	1939	4	US-09-949-016-11104	Sequence 11104, A
32	102	9.7	281	4	US-09-914-259-45	Sequence 45, Appl
33	102	9.7	284	4	US-09-914-259-47	Sequence 47, Appl
34	102	9.7	284	4	US-09-914-259-57	Sequence 57, Appl
35	102	9.7	372	1	US-07-813-584A-3	Sequence 3, Appl
36	102	9.7	372	1	US-08-330-515-3	Sequence 3, Appl
37	102	9.7	1031	4	US-09-914-259-24	Sequence 24, Appl
38	102	9.7	1940	4	US-09-538-092-901	Sequence 901, Appl
39	102	9.7	1963	4	US-09-949-016-8888	Sequence 8888, Ap
40	101.5	9.7	2662	4	US-09-595-684B-31	Sequence 31, Appl
41	101.5	9.7	2663	4	US-09-538-092-1252	Sequence 1252, Ap
42	100.5	9.6	284	4	US-09-914-259-59	Sequence 59, Appl
43	100	9.6	1104	3	US-08-923-992A-4	Sequence 4, Appl
44	100	9.6	1164	3	US-08-923-992A-10	Sequence 10, Appl
45	99.5	9.5	588	4	US-08-714-741-42	Sequence 42, Appl

ALIGNMENTS

```

RESULT 1
US-09-621-976-4959
; Sequence 4959, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jober, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTS and Encoded Human Proteins.
; FILE REFERENCE: GENET. 054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 4959
; LENGTH: 127
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-621-976-4959

Query Match      56.7%; Score 593.5; DB 4; Length 127;
Best Local Similarity 89.6%; Pred. No. 1.7e-50;
Matches 120; Conservative 5; Mismatches 2; Indels 7; Gaps 1;

QY      1 MSKKGSLAEKRTMMEIFSETKVFOLKDIKIAPEKGTITAMSVKEVLSDVDGMY 60
      |||
DB      1 MSKKGSLAEKRTMMEIFSETKVFOLKDIKIAPEKGTITAMSVKEVLSDVDGMY 60

QY      61 DERIGTSNYVYAFPSKALHARKHLEVLSEGLSGSQHSLQSIKAKIGRCETERR 120
      |||
DB      61 DERIGTSNYVYAFPSKALHARKHLEVLSEGLSGSQHSLQSIKAKIGRCETERR 117

QY      121 TRLAKELSLRDPOR 134
      |||
DB      118 ----IKLSGMQBER 127

RESULT 2
US-09-248-796A-14485
; Sequence 14485, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstein et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13

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PRIOR APPLICATION NUMBER: US 60/096,409
 PRIOR FILING DATE: 1998-08-13
 NUMBER OF SEQ ID NOS: 28208
 SEQ ID NO: 14485
 LENGTH: 260
 TYPE: PRP
 ORGANISM: Candida albicans
 US-09-248-796A-14485

Query Match
 Best Local Similarity 18.3%; Score 191.5; DB 4; Length 260;
 Matches 59; Conservative 47; Mismatches 75; Indels 37; Gaps 8;

QY 1 MSKKGLSABEKRTMEIFSETKDVOLKLEKIAPEKGTITAMSVKVLQSLVDGMDV 60
 DB 60 MPKKGTLDEETKLSALWFMOSDMFTYLAKEISKASKOCKIPPMOMELVALVERGLV 119
 QY 61 DCRIGTSNYWAFPSKALHARKKLEVLSSQLSESGOHAJLOKSIKAK-----IGR 114
 DB 120 EDRCGCTTNLYMSFP-----YLOHKQ-----QETHRLNRTIANLETERDSLICH 165
 QY 115 C-ETEBRTLAKELSLR-----DOROLKAEVETKCDPOVEEIRPOANKVAKKA 166
 DB 166 CKDITGVNQTHERASAKIRFCQOSLERIDSIOSQLOKSES--VE-----NLVTSIAF 218
 QY 167 NRTWDNIFAIKSWAKKFGFEENKIDRTFGIPEDFDYI 204
 DB 219 --PSDSIDILICVLSHQGLTWTITKTEFELPLEFEERI 254

RESULT 3
 US-09-538-092-1321
 Sequence 1321, Application US/09538092
 Patent No. 6753314
 GENERAL INFORMATION:
 APPLICANT: Manfield, Tracy A.
 TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
 FILE REFERENCE: 15966-542
 CURRENT APPLICATION NUMBER: US/09/538,092
 PRIOR FILING DATE: 2000-03-29
 PRIOR APPLICATION NUMBER: 60/127,352
 PRIOR FILING DATE: 1999-04-01
 PRIOR APPLICATION NUMBER: 60/178,965
 NUMBER OF SEQ ID NOS: 1387
 SOFTWARE: CurapatSeqFormat Version 0.9
 SEQ ID NO: 1321
 LENGTH: 1270
 TYPE: PRP
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (0)...(0)
 OTHER INFORMATION: Polypeptide Accession Number, Q14203
 US-09-538-092-1321

Query Match
 Best Local Similarity 12.8%; Score 134.5; DB 4; Length 1270;
 Matches 50; Conservative 43; Mismatches 106; Indels 15; Gaps 5;

QY 2 SKKGLSABEKRTMEIFSETKDVOLKLEKIAPEKGTITAMSVKVLQSLVDGMDV 61
 DB 271 AKEKKEALFAKERMEHMDTADALEMATLDEKMAEERASLSQEVVALKERYDELTTD 330
 QY 62 CERI-----GTSNYWAFPSKALHAR-KHKLVLSSQLSESGOHAJLOKSIKAK 110
 DB 331 LEILKALIEKSGSQAASSYOLKQLEEQVARKKALVNRDLSSSEKQEHVKLOKLMER- 389
 QY 111 KIGRCE--ERTLAKELSLRDOROLKAEVETKCDPOVEEIRPOANKVAKKAANR 168
 DB 390 KNOLELVNQORRLOEELSQAESTIDELKQVDAALGAE-EMVETLTRNINLSEKVE 448

QY 169 WTDNIFAIKSWAKKFGFEENKIDRTFGIPEDFD 202
 DB 449 LRETVGDLEANNMNDLEQENARFETLELEQD 482

RESULT 4
 US-09-104-324B-4
 Sequence 4, Application US/09104324B
 Patent No. 6232460
 GENERAL INFORMATION:
 APPLICANT: T rec1, Ozlem; Sahin, Ugur; Pfeundschuh, Michael
 TITLE OF INVENTION: Methods For Diagnosis And Treating Cancers,
 TITLE OF INVENTION: And Methods For Identifying Pathogenic Markers In A Sample Of
 NUMBER OF SEQUENCES: 4
 CORRESPONDENCE ADDRESSES:
 ADDRESSER: Fulbright & Jaworski LLP
 STREET: 666 Fifth Avenue
 CITY: New York City
 STATE: New York
 ZIP: 10103

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
 COMPUTER: IBM
 OPERATING SYSTEM: PC-DOS
 SOFTWARE: Wordperfect
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/104,324B
 FILING DATE: 25-June-1998
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/892,702
 FILING DATE: 15-July-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Hanson, No. 6232460man D.
 REGISTRATION NUMBER: 30,946
 REFERENCE/DOCKET NUMBER: LUD 5491
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 752-5958
 TELEFAX: (212) 318-3000
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 976 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 US-09-104-324B-4

Query Match
 Best Local Similarity 11.2%; Score 117; DB 3; Length 976;
 Matches 63; Conservative 38; Mismatches 85; Indels 78; Gaps 13;

QY 3 KKKGLSABE-KRTIMEI-FSETKDV-----FOLKLEKIAPEKGTITAMSVKVEV 51
 DB 413 QKSSSELEEMTKLNNKEVELEBKVLGEKETLLYENKQPEKIAELKQ-TEOELIGLL 471
 QY 52 QSL---VDDGMDVCEIGTSNYWAFPSKAL-----HARKKLEVL-- 90
 DB 472 QAREKEVHLEQLTRATITSEQYSKEVYKDLTELENEKAKTELTSNCKKLSTNKEIT 531
 QY 91-----SOLSESGOHAJLOKSIKAKIGRCEETERTLAKELSLRDOROL 136
 DB 532 QETSDMTLELKNQOEDINNKKOEERMLKOIE--NLQETETOLRNELEVEVEELKQKRD 589
 QY 137 LKAEVEKTKD-CD-----POVEEIRPOANKVAKK--ANRWTNDIIFAIK----- 177
 DB 590 VKCKDKSSEENCNLRQOVENKRYTIEELQOENKALKKKGTAESKQJNVYIKVNTKLE 649
 QY 178 -SWAKKFG-----PEENKI 191
 DB 650 LESAKOKFGELITTYOKETEDK 673

RESULT 5

US-09-538-092-1339
 ; Sequence 1339, Application US/09538092
 ; Patent No. 6753314
 ; GENERAL INFORMATION:
 ; APPLICANT: Giot, Loic
 ; APPLICANT: Mansfield, Traci A.
 ; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
 ; FILE REFERENCE: 15966-542
 ; CURRENT FILING DATE: 2000-03-29
 ; PRIOR FILING DATE: 1999-04-01
 ; PRIOR APPLICATION NUMBER: 60/127,352
 ; PRIOR FILING DATE: 2000-02-01
 ; NUMBER OF SEQ ID NOS: 1387
 ; SOFTWARE: CuraPatSeqFormatter Version 0.9
 ; SEQ ID NO: 1339
 ; LENGTH: 976
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (0)...(0)
 ; OTHER INFORMATION: Polypeptide Accession Number Q15431
 US-09-538-092-1339

Query Match 11.2%; Score 117; DB 4; Length 976;
 Best Local Similarity 23.9%; Pred. No. 0.0099;
 Matches 63; Conservative 38; Mismatches 85; Indels 78; Gaps 13;

QY 3 KKKGISAE--KRTMMEI-FSETRDV-----FOLKLEKIAPEKIGITAMSVKEVL 51
 DB 413 OKKSELEBMTLTNNKEVELELKKVGEKETLLYENKQFPIAELKLG-TEQELIGLL 471
 QY 52 OSL--VDDGWDICRIGTSNYTAPPSKAL-----HARKKLEVL-- 90
 DB 472 QAREKEVHDLQLTAITTSQYYSKEVDLTELLENKLTNTELTSHCNKLTLENKELT 531
 QY 91 -----SOLSEGSOKHASLOKSIKAKIGRCETERTRLAKELSLRDORQ 136
 DB 532 QETSMTELEKNOQEDINNKKQBERMLKQIE--NIQETITQRLBLEYREELKQKDE 589
 QY 137 LKAEEKYKD-CD-----POVVEIRQANKVAKE--AANRWTDNIFAIK----- 177
 DB 590 VKCKLDKSEBNCNNLRKQVENNKYIEELQGENKALKKKGTASBKQLANYEIKVKNLELE 649
 QY 178 -SWAKRFG-----PEENKI 191
 DB 650 LESAKQKFGIEITDYQKEIEDKKI 673

RESULT 6
 US-09-914-259-55
 ; Sequence 55, Application US/09914259
 ; Patent No. 6495336
 ; GENERAL INFORMATION:
 ; APPLICANT: Makowski, Lee
 ; APPLICANT: Hyman, Paul
 ; APPLICANT: Williams, Mark
 ; TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES
 ; FILE REFERENCE: 8471-010-999
 ; CURRENT FILING DATE: 2000-11-21
 ; NUMBER OF SEQ ID NOS: 180
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO: 55
 ; LENGTH: 284
 ; TYPE: PRT
 ; ORGANISM: Sus scrofa
 US-09-914-259-55

Query Match 10.9%; Score 114; DB 4; Length 284;
 Best Local Similarity 23.2%; Pred. No. 0.0037;

Matches 52; Conservative 37; Mismatches 61; Indels 74; Gaps 11;
 QY 1 MSKKGLSAE--EKRTMMEIFSETKQVFOLEKLEKIAPEKIGITAMSVKEVLQSLVD 57
 DB 73 LAEKATADBADVASINRRIQLFEELDRQA-----ERLA-----TALQKEBAKRADE 122
 QY 58 ---GNVDCERIGTSNYTAPPSKALHAR---KHLVLESQSLSEGSQK----- 100
 DB 123 SERGM-----KVIESRAQKDEBEMIEIOELQKEA--KHIAEDADRKYE 163
 QY 101 -----ASLOKSIKAKI--GRCTEERTRLAKELSLRDORQKAEVEKYKD 148
 DB 164 EVARLVITIEESDLERAEERAEISEGKC-----AELEBELKVTNNLSLEAQAEKYSQKE 218
 QY 149 POVVEIRQANKVAKEAANRWTDNIFAIKSWAKRFGPEENKID 192
 DB 219 DKVEEIKVLSDKLEAETR-----AEPRERSVTLEKSID 254

RESULT 7
 US-09-914-259-62
 ; Sequence 62, Application US/09914259
 ; Patent No. 6495336
 ; GENERAL INFORMATION:
 ; APPLICANT: Makowski, Lee
 ; APPLICANT: Hyman, Paul
 ; APPLICANT: Williams, Mark
 ; TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES
 ; FILE REFERENCE: 8471-010-999
 ; CURRENT FILING DATE: 2000-11-21
 ; NUMBER OF SEQ ID NOS: 180
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO: 62
 ; LENGTH: 284
 ; TYPE: PRT
 ; ORGANISM: Rattus norvegicus
 US-09-914-259-62

Query Match 10.8%; Score 113.5; DB 4; Length 284;
 Best Local Similarity 21.1%; Pred. No. 0.0042;
 Matches 48; Conservative 48; Mismatches 78; Indels 53; Gaps 8;

QY 2 SKKKLSA--EERKTMMEIFSETKQVFOLEKLEKIAPEKIGITAMSVK-EVLQSLVDGM 59
 DB 45 AKERLLRSBDBRDRVLELHKAEDSLAAD-ETAKKADBADVASINRRIQLVEELDRQA 103
 QY 60 VDCERIGTSNYTAPPSKALHARKKLEVLSEGSQK----- 99
 DB 104 ---ERLATALQKLEBAKRADESERGMKVIESRAQKDEKEMIEIOELQKEAHHIAEDADR 160
 QY 100 -----HASLOKSIKAKI--GRCTEERTRLAKELSLRDORQKAEVEKYK 145
 DB 161 KYEVARLVITIEESDLERAEERAEISEGKC-----AELEBELKVTNNLSLEAQAEKYS 215
 QY 146 DCDPOVVEIRQANKVAKEAANRWTDNIFAIKSWAKRFGPEENKID 192
 DB 216 QKEDKYEIEIKVLSDKLEAETR-----AEPRERSVTLEKSID 254

RESULT 8
 US-09-248-796A-20275
 ; Sequence 20275, Application US/09248796A
 ; Patent No. 6747137
 ; GENERAL INFORMATION:
 ; APPLICANT: Keith Weinstein et al
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
 ; FILE REFERENCE: 107196.132
 ; CURRENT FILING DATE: 1999-02-12
 ; PRIOR APPLICATION NUMBER: US 60/074,725
 ; PRIOR FILING DATE: 1998-02-13

Thu Mar 24 08:29:11 2005

us-10-087-190-3.ral

PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 20275
; LENGTH: 630
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-20275

Query Match
Best Local Similarity 10.7%; Score 112.5; DB 4; Length 630;
Matches 49; Conservative 43; Mismatches 79; Indels 35; Gaps 8;

QY 3 KKKLSAEKRTMMEIFSETKDVQPOLDEKIAPKREKGT--AMSVKVLQSLVDGAV 60
DB 158 KTKNSDTELEKQLELEKVK-----IDLQADEKLGITTEIRILKSELETVNSG-- 210
QY 61 DCRIGTSNYWAFPS--KALHARKHLELV-----BSQSEGSOKIASLOKSI----- 107
DB 211 -LSTTELALTKTVKSLKEKEKELOFLSNKSKLELDYIOGHSDISEKALYDEL 266
QY 108 -EKATIGCEETEERTRLAKELSLRDQREQLAEVEKYKCDPQVVEIRQANKVAKAA 166
DB 267 KEKTQFDPSKKKLTLENDLITKKELETKTQTSKFKNLERRKDEIVAKNELELTK 326
QY 167 NRTWDNIFAIKSMARKRFFGEHKKID 192
DB 327 N--DN-----SGAKTELEKVKSLKE 344

RESULT 9

US-09-914-259-43
; Sequence 43; Application US/09914259
; Patent No. 6495336
; GENERAL INFORMATION:
; APPLICANT: Makowski, Lee
; APPLICANT: Hyman, Paul
; TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES
; FILE REFERENCE: 8471-010-999
; CURRENT APPLICATION NUMBER: US/09/914,259
; CURRENT FILING DATE: 2000-11-21
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 43
; LENGTH: 284
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-914-259-43

Query Match
Best Local Similarity 10.7%; Score 112; DB 4; Length 284;
Matches 52; Conservative 41; Mismatches 72; Indels 56; Gaps 9;

QY 1 MSKKKGLSABEK--RTMMEIFSETKDVQ-----LKOLEKIAPK-EKGTAMSV 47
DB 73 LAEKKAADAEVASLNRIQLVEEELDRQERLATATLQLEAEKAADESRGKMYEN 132
QY 48 KEVLQSLVDGMDVDERIGTSNYWAFPSKALHARKHLELVESQSEGSOKIASLOKSI 107
DB 133 R-----ALNDEEKEMLQEI-----OLKEAGHAEALRYEVAKLVIIIGDL 176
QY 108 EKAKIGCEETEERTLA-----KELSLRDQREQLAEVEKYKCDPQVVEIRQANK 159
DB 177 EK-----TERAELESKCSLEELNKNVNNIKSLAEAKESQCEDEYEEIKILT 229
QY 160 KVAAEANRTWDNIFAIKSMARKRFFGEHKKIDRTFFGIPED 200
DB 230 DKLKEATRAE--FAERSVA-----KLEKTIIDDLSD 258

RESULT 10
US-09-538-092-918

Sequence 918; Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Glot, Loic
; APPLICANT: Mansfield, Tracy A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-942
; CURRENT APPLICATION NUMBER: US/09/538,092
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CuraPatSeqFormatter Version 0.9
; SEQ ID NO 918
; LENGTH: 1937
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0).....(0)
; OTHER INFORMATION: Polypeptide Accession Number P13535
US-09-538-092-918

Query Match
Best Local Similarity 10.6%; Score 111; DB 4; Length 1937;
Matches 54; Conservative 42; Mismatches 88; Indels 50; Gaps 9;

QY 4 KKKLSAEKRTMMEIFSETKDVQPOLDEKIAPK-----EKGTAMSV-----V 47
DB 1361 ORALSKANSEVAVQMKRYETDAIORTLELEAKKLAQRLQAEHVAVAKASLEKT 1420
QY 48 KEVLQSLVDGMDVDERIGTS-----NYWAFPSKALHARKHLELVESQSEGS 98
DB 1421 KORQNEVEDMDLVERSNAACAALDKORNF-----DKVLEWKQYESTOMELASOK 1475
QY 99 KHALQSIKAK-----IGRCET--EERTRLAKELSLRD-----RQQLKAE 140
DB 1476 ESRSLSTELFKVKNVEESLDQLETLRENNKILQOETISDLTBIAAGQIHELKIKQ 1535
QY 141 VEKYKCDPQVVEIRQANKVAKAA-ANRTWDNIFAIKSMARKRFFGEHKKIDR 193
DB 1536 VEOEK-CEIQALAEAEASLEHEGKITRIQLTLNQVSEVDRKIAERDEIDQ 1588

RESULT 11

US-09-914-259-46
; Sequence 46; Application US/09914259
; Patent No. 6495336
; GENERAL INFORMATION:
; APPLICANT: Makowski, Lee
; APPLICANT: Hyman, Paul
; TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES
; FILE REFERENCE: 8471-010-999
; CURRENT APPLICATION NUMBER: US/09/914,259
; CURRENT FILING DATE: 2000-11-21
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 46
; LENGTH: 284
; TYPE: PRT
; ORGANISM: Brachydanio rerio
US-09-914-259-46

Query Match
Best Local Similarity 10.5%; Score 110; DB 4; Length 284;
Matches 51; Conservative 44; Mismatches 72; Indels 52; Gaps 10;

QY 1 MSKKKGLSABEK--ERTMMEIFSETKDVQ-----LKOLEKIAPK-EKGTAMSV 47
DB 73 LAEKKAADAEVASLNRIQLVEEELDRQERLATATLQLEAEKAADESRGKMYEN 132

us-10-087-190-3.ra1

```

1  APPLICANT: Keith Weinstein et al
2  TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
3  FILE REFERENCE: 107196.112
4  CURRENT APPLICATION NUMBER: US/09/248,796A
5  PRIOR APPLICATION NUMBER: 1999-02-12
6  PRIOR FILING DATE: 1998-02-13
7  PRIOR APPLICATION NUMBER: US 60/074,725
8  PRIOR FILING DATE: 1998-08-13
9  NUMBER OF SEQ ID NOS: 28208
10 SEQ ID NO 20276
11 LENGTH: 817
12 TYPE: PRT
13 ORGANISM: Candida albicans
14 US-09-248-796A-20276

```

Qy 5 ABEKTRMEIFSETKVOPOLKLEKIAPREKINGYMSVK--EVLGSUV---DGWDOCE 63
Db ||||| : : : : :
426 ABEKOV..LIDBKENNDRIDTEAEKIAARKOESEIQAEDKLFTPTDEIKESAKLE 484
Qy ||||| : : : : :
64 RIGTSNYMFPSPKAH-----ARKKLTVEVLSQSOSQHASLOKSIEKANIGRCETEE 119
Db ||||| : : : : :
485 EVMARDELANEVMAVEDLNKEYEKLAETESKOQEMANDIEKYTTDIEEA-----TAK 538
Qy ||||| : : : : :
120 RTTLAWEISLDQBEOULKAVER..YDCOPVVEELROANKVAREANRWTDNIPAIKS 178
Db ||||| : : : : :
539 HESTDEVAVELOETHDEKEDAKAEKHEDLEDGKLEEBEKOKUHLTEDKATTKKKDLAAITE 598
Qy ||||| : : : : :
179 MAKRFGEENKIDPITSGIPE 199
Db ||||| : : : : :
599 KVK-----DEKINSE--LPE 612

Search completed: March 23, 2005, 19:19:27
Job time : 44 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model.

Run on: March 23, 2005, 19:17:58 ; Search time 138 Seconds
(without alignments)
491.853 Million cell updates/sec

Title: US-10-087-190-3

Perfect score: 1047
Sequence: 1 MSKKKGLSAEKRTRMEIF.....FEENKIDRTFGIPEDFDYID 205

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1407402 seqs, 331100923 residues

Total number of hits satisfying chosen parameters: 1407402

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications AA.*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
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9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_NEW_PUB.pep.*
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14: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1047	100.0	205	US-09-799-250-2	Sequence 2, Appli
2	1047	100.0	205	US-10-087-190-3	Sequence 3, Appli
3	1047	100.0	205	US-10-087-190-14	Sequence 14, Appli
4	1047	100.0	205	US-10-087-190-20	Sequence 20, Appli
5	1047	100.0	205	US-10-087-190-21	Sequence 21, Appli
6	1047	100.0	205	US-10-087-190-22	Sequence 22, Appli
7	1047	100.0	205	US-10-087-190-61	Sequence 61, Appli
8	1047	100.0	205	US-10-408-765A-1821	Sequence 1821, Ap
9	1036.5	99.0	206	US-10-087-190-44	Sequence 44, Appli
10	1036.5	99.0	206	US-10-087-190-45	Sequence 45, Appli
11	1011	96.6	198	US-10-087-190-24	Sequence 24, Appli
12	975	93.1	190	US-10-087-190-13	Sequence 13, Appli
13	975	93.1	190	US-10-087-190-19	Sequence 19, Appli

14	975	93.1	190	US-10-087-190-67	Sequence 67, Appli
15	975	93.1	190	US-10-087-190-68	Sequence 68, Appli
16	975	93.1	190	US-10-087-190-69	Sequence 69, Appli
17	948	90.5	205	US-09-799-250-4	Sequence 4, Appli
18	948	90.5	205	US-10-087-190-23	Sequence 23, Appli
19	945.5	90.3	190	US-10-087-190-11	Sequence 11, Appli
20	945.5	90.3	190	US-10-087-190-18	Sequence 18, Appli
21	945.5	90.3	190	US-10-087-190-62	Sequence 62, Appli
22	945.5	90.3	190	US-10-087-190-63	Sequence 63, Appli
23	614	58.6	122	US-10-087-190-53	Sequence 53, Appli
24	591	56.4	122	US-10-087-190-9	Sequence 9, Appli
25	591	56.4	122	US-10-087-190-17	Sequence 17, Appli
26	591	56.4	122	US-10-087-190-54	Sequence 54, Appli
27	591	56.4	122	US-10-087-190-55	Sequence 55, Appli
28	584	55.8	119	US-10-087-190-7	Sequence 7, Appli
29	584	55.8	119	US-10-087-190-16	Sequence 16, Appli
30	584	55.8	119	US-10-087-190-47	Sequence 47, Appli
31	465	44.4	126	US-10-087-190-5	Sequence 5, Appli
32	465	44.4	126	US-10-087-190-15	Sequence 15, Appli
33	465	44.4	126	US-10-087-190-46	Sequence 46, Appli
34	427	40.8	207	US-10-437-963-162899	Sequence 162899,
35	394	37.6	235	US-10-437-963-162901	Sequence 162901,
36	349	33.3	200	US-09-799-250-5	Sequence 5, Appli
37	349	33.3	200	US-10-087-190-25	Sequence 25, Appli
38	287	27.4	79	US-10-106-698-5443	Sequence 5443, Ap
39	255.5	24.4	218	US-10-083-357-1304	Sequence 1304, Ap
40	214.5	20.5	74	US-10-424-599-192650	Sequence 192650,
41	121.5	11.6	715	US-10-408-765A-2096	Sequence 2096, Ap
42	121.5	11.6	1881	US-10-032-585-7646	Sequence 7646, Ap
43	120.5	11.5	1798	US-09-981-151A-48	Sequence 48, Appli
44	117	11.2	795	US-10-408-765A-1205	Sequence 1205, Ap
45	117	11.2	795	US-10-416-330-34	Sequence 34, Appli

ALIGNMENTS

RESULT 1
US-09-799-250-2
; Sequence 2, Application US/09799250
; Publication No. US20030032087A1
; GENERAL INFORMATION:
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Rene S. Hubert
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Arthur B. Raicano
; APPLICANT: Mary Faris
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: HIGHLY EXPRESSED IN VARIOUS CANCERS
; FILE REFERENCE: 129.34US01
; CURRENT APPLICATION NUMBER: US/09/799,250
; CURRENT FILING DATE: 2001-02-08
; NUMBER OF SEQ ID NOS: 719
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 205
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-799-250-2

Query Match	100.0%	Score 1047;	DB 10;	Length 205;
Best Local Similarity	100.0%	Pred. NO. 3e-78;		
Matches 205;	Conservative	0;	Mismatches 0;	Indels 0;
Gap 0;				
QY	1	MSKKKGLSAEKRTRMEIFSETKVFQIKDKETAPKEKGTITAMSVKVLQSLVDGAV	60	
DB	1	MSKKKGLSAEKRTRMEIFSETKVFQIKDKETAPKEKGTITAMSVKVLQSLVDGAV	60	
QY	61	DERIGTSTNYTAAFPSSKALHARKKLEVLSEGLSGSQSHASLOKSIERAKTIGRCETTER	120	
DB	61	DERIGTSTNYTAAFPSSKALHARKKLEVLSEGLSGSQSHASLOKSIERAKTIGRCETTER	120	

QY 121 TRAKELSLRDQREOLKAVERKDCDPVVEEIRONAKVAKAANRWTDNIFAISMA 180
 DB 121 TRAKELSLRDQREOLKAVERKDCDPVVEEIRONAKVAKAANRWTDNIFAISMA 180
 QY 181 KRKGFEEENKIDRTFGIPEDFDYID 205
 DB 181 KRKGFEEENKIDRTFGIPEDFDYID 205

RESULT 2

US-10-087-190-3
 ; Sequence 3 Application US/10087190
 ; Publication No. US20030223997A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Agensys, Inc.
 ; APPLICANT: Chailita-Bid, Pia M.
 ; APPLICANT: Hubert, Rene S.
 ; APPLICANT: Raitano, Arthur B.
 ; APPLICANT: Paris, Mary
 ; APPLICANT: Afar, Daniel E. H.
 ; APPLICANT: Ge, Wangmao
 ; APPLICANT: Jakobovitz, Aya
 ; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
 ; FILE REFERENCE: ENTITLED 121P1F1 USEFUL IN TREATMENT AND DETECTION OF CANCER
 ; CURRENT APPLICATION NUMBER: US/10/087,190
 ; PRIOR FILING DATE: 2003-01-28
 ; PRIOR FILING DATE: 2001-03-05
 ; NUMBER OF SEQ ID NOS: 69
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 3
 ; LENGTH: 205
 ; TYPE: PRT
 ; ORGANISM: Homo Sapiens
 US-10-087-190-3

Query Match
 Best Local Similarity 100.0%; Score 1047; DB 15; Length 205;
 Matches 205; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSKKKGLSAEERTMMEIFSETDVOLKDLKIAPKKGTITAMSVKVEVLSLVDDGMV 60
 DB 1 MSKKKGLSAEERTMMEIFSETDVOLKDLKIAPKKGTITAMSVKVEVLSLVDDGMV 60
 QY 61 DCRIGTSNYWAFPSKALHARKHKLVEVLSQISEGSGQHASLQSIKAKIGRCETEER 120
 DB 61 DCRIGTSNYWAFPSKALHARKHKLVEVLSQISEGSGQHASLQSIKAKIGRCETEER 120
 QY 121 TRAKELSLRDQREOLKAVERKDCDPVVEEIRONAKVAKAANRWTDNIFAISMA 180
 DB 121 TRAKELSLRDQREOLKAVERKDCDPVVEEIRONAKVAKAANRWTDNIFAISMA 180
 QY 181 KRKGFEEENKIDRTFGIPEDFDYID 205
 DB 181 KRKGFEEENKIDRTFGIPEDFDYID 205

RESULT 3

US-10-087-190-14
 ; Sequence 14 Application US/10087190
 ; Publication No. US20030223997A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Agensys, Inc.
 ; APPLICANT: Chailita-Bid, Pia M.
 ; APPLICANT: Hubert, Rene S.
 ; APPLICANT: Raitano, Arthur B.
 ; APPLICANT: Paris, Mary
 ; APPLICANT: Afar, Daniel E. H.
 ; APPLICANT: Ge, Wangmao
 ; APPLICANT: Jakobovitz, Aya
 ; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN

;; TITLE OF INVENTION: ENTITLED 121P1F1 USEFUL IN TREATMENT AND DETECTION OF CANCER
 ;; FILE REFERENCE: 51158-20034.20
 ;; CURRENT APPLICATION NUMBER: US/10/087,190
 ;; PRIOR FILING DATE: 2003-01-28
 ;; PRIOR FILING DATE: 2001-03-05
 ;; NUMBER OF SEQ ID NOS: 69
 ;; SOFTWARE: FastSeq for Windows Version 4.0
 ;; SEQ ID NO 14
 ;; LENGTH: 205
 ;; TYPE: PRT
 ;; ORGANISM: Homo Sapiens
 US-10-087-190-14

Query Match
 Best Local Similarity 100.0%; Score 1047; DB 15; Length 205;
 Matches 205; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSKKKGLSAEERTMMEIFSETDVOLKDLKIAPKKGTITAMSVKVEVLSLVDDGMV 60
 DB 1 MSKKKGLSAEERTMMEIFSETDVOLKDLKIAPKKGTITAMSVKVEVLSLVDDGMV 60
 QY 61 DCRIGTSNYWAFPSKALHARKHKLVEVLSQISEGSGQHASLQSIKAKIGRCETEER 120
 DB 61 DCRIGTSNYWAFPSKALHARKHKLVEVLSQISEGSGQHASLQSIKAKIGRCETEER 120
 QY 121 TRAKELSLRDQREOLKAVERKDCDPVVEEIRONAKVAKAANRWTDNIFAISMA 180
 DB 121 TRAKELSLRDQREOLKAVERKDCDPVVEEIRONAKVAKAANRWTDNIFAISMA 180
 QY 181 KRKGFEEENKIDRTFGIPEDFDYID 205
 DB 181 KRKGFEEENKIDRTFGIPEDFDYID 205

RESULT 4

US-10-087-190-20
 ; Sequence 20 Application US/10087190
 ; Publication No. US20030223997A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Agensys, Inc.
 ; APPLICANT: Chailita-Bid, Pia M.
 ; APPLICANT: Hubert, Rene S.
 ; APPLICANT: Raitano, Arthur B.
 ; APPLICANT: Paris, Mary
 ; APPLICANT: Afar, Daniel E. H.
 ; APPLICANT: Ge, Wangmao
 ; APPLICANT: Jakobovitz, Aya
 ; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
 ; FILE REFERENCE: ENTITLED 121P1F1 USEFUL IN TREATMENT AND DETECTION OF CANCER
 ; CURRENT APPLICATION NUMBER: US/10/087,190
 ; PRIOR FILING DATE: 2003-01-28
 ; PRIOR FILING DATE: 2001-03-05
 ; NUMBER OF SEQ ID NOS: 69
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 20
 ; LENGTH: 205
 ; TYPE: PRT
 ; ORGANISM: Homo Sapiens
 US-10-087-190-20

Query Match
 Best Local Similarity 100.0%; Score 1047; DB 15; Length 205;
 Matches 205; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSKKKGLSAEERTMMEIFSETDVOLKDLKIAPKKGTITAMSVKVEVLSLVDDGMV 60
 DB 1 MSKKKGLSAEERTMMEIFSETDVOLKDLKIAPKKGTITAMSVKVEVLSLVDDGMV 60
 QY 61 DCRIGTSNYWAFPSKALHARKHKLVEVLSQISEGSGQHASLQSIKAKIGRCETEER 120
 DB 61 DCRIGTSNYWAFPSKALHARKHKLVEVLSQISEGSGQHASLQSIKAKIGRCETEER 120

Db 61 DCRIGTSNYWAFPSKALHARKHLEVLSEQLSEGSQGHASLOKSIERAKIGRCETTER 120
Qy 121 TRLAKELSLRQROQLKAEVEKYKDCDPQVVEIRQANKVKAANRWTDNIFAIXSWA 180
Db 121 TRLAKELSLRQROQLKAEVEKYKDCDPQVVEIRQANKVKAANRWTDNIFAIXSWA 180
Qy 181 KRKFGFEENKIDRTGIPEDFDYID 205
Db 181 KRKFGFEENKIDRTGIPEDFDYID 205

RESULT 5

US-10-087-190-21
; Sequence 21, Application US/10087190
; Publication No. US20030223997A1
; GENERAL INFORMATION:

; APPLICANT: Agensys, Inc.
; APPLICANT: Challita-Bid, Pia M.
; APPLICANT: Hubert, Rene S.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Afar, Daniel E. H.
; APPLICANT: Ge, Wangmao
; APPLICANT: Jakobovitz, Aya
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
; TITLE OF INVENTION: ENTITLED 121P1P1 USEFUL IN TREATMENT AND DETECTION OF CANCER
; FILE REFERENCE: 51158-20034.20
; CURRENT APPLICATION NUMBER: US/10/087,190
; CURRENT FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: US 09/779,250
; PRIOR FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 205
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-087-190-21

Query Match 100.0%; Score 1047; DB 15; Length 205;

Best Local Similarity 100.0%; Pred. No. 3e-78; Indels 0; Gaps 0;

Matches 205; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 61 DCRIGTSNYWAFPSKALHARKHLEVLSEQLSEGSQGHASLOKSIERAKIGRCETTER 120
Db 61 DCRIGTSNYWAFPSKALHARKHLEVLSEQLSEGSQGHASLOKSIERAKIGRCETTER 120
Qy 121 TRLAKELSLRQROQLKAEVEKYKDCDPQVVEIRQANKVKAANRWTDNIFAIXSWA 180
Db 121 TRLAKELSLRQROQLKAEVEKYKDCDPQVVEIRQANKVKAANRWTDNIFAIXSWA 180
Qy 181 KRKFGFEENKIDRTGIPEDFDYID 205
Db 181 KRKFGFEENKIDRTGIPEDFDYID 205

RESULT 6

US-10-087-190-22
; Sequence 22, Application US/10087190
; Publication No. US20030223997A1
; GENERAL INFORMATION:

; APPLICANT: Agensys, Inc.
; APPLICANT: Challita-Bid, Pia M.
; APPLICANT: Hubert, Rene S.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Afar, Daniel E. H.
; APPLICANT: Ge, Wangmao
; APPLICANT: Jakobovitz, Aya

; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
; TITLE OF INVENTION: ENTITLED 121P1P1 USEFUL IN TREATMENT AND DETECTION OF CANCER
; FILE REFERENCE: 51158-20034.20
; CURRENT APPLICATION NUMBER: US/10/087,190
; CURRENT FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: US 09/779,250
; PRIOR FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 205
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-087-190-22

Query Match 100.0%; Score 1047; DB 15; Length 205;

Best Local Similarity 100.0%; Pred. No. 3e-78; Indels 0; Gaps 0;

Matches 205; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSKKKGLSABEKRRTMEIFSETKDVFOQLDEKIAPEKEGITTANSVKEVLQSLVDDGNV 60
Db 1 MSKKKGLSABEKRRTMEIFSETKDVFOQLDEKIAPEKEGITTANSVKEVLQSLVDDGNV 60
Qy 61 DCRIGTSNYWAFPSKALHARKHLEVLSEQLSEGSQGHASLOKSIERAKIGRCETTER 120
Db 61 DCRIGTSNYWAFPSKALHARKHLEVLSEQLSEGSQGHASLOKSIERAKIGRCETTER 120
Qy 121 TRLAKELSLRQROQLKAEVEKYKDCDPQVVEIRQANKVKAANRWTDNIFAIXSWA 180
Db 121 TRLAKELSLRQROQLKAEVEKYKDCDPQVVEIRQANKVKAANRWTDNIFAIXSWA 180
Qy 181 KRKFGFEENKIDRTGIPEDFDYID 205
Db 181 KRKFGFEENKIDRTGIPEDFDYID 205

RESULT 7

US-10-087-190-61
; Sequence 61, Application US/10087190
; Publication No. US20030223997A1
; GENERAL INFORMATION:

; APPLICANT: Agensys, Inc.
; APPLICANT: Challita-Bid, Pia M.
; APPLICANT: Hubert, Rene S.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Afar, Daniel E. H.
; APPLICANT: Ge, Wangmao
; APPLICANT: Jakobovitz, Aya
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
; TITLE OF INVENTION: ENTITLED 121P1P1 USEFUL IN TREATMENT AND DETECTION OF CANCER
; FILE REFERENCE: 51158-20034.20
; CURRENT APPLICATION NUMBER: US/10/087,190
; CURRENT FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: US 09/779,250
; PRIOR FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 61
; LENGTH: 205
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-087-190-61

Query Match 100.0%; Score 1047; DB 15; Length 205;

Best Local Similarity 100.0%; Pred. No. 3e-78; Indels 0; Gaps 0;

Matches 205; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSKKKGLSABEKRRTMEIFSETKDVFOQLDEKIAPEKEGITTANSVKEVLQSLVDDGNV 60
Db 1 MSKKKGLSABEKRRTMEIFSETKDVFOQLDEKIAPEKEGITTANSVKEVLQSLVDDGNV 60
Qy 61 DCRIGTSNYWAFPSKALHARKHLEVLSEQLSEGSQGHASLOKSIERAKIGRCETTER 120

```

Db      61 DCRIGTSNYWAFPSKALHARKHKLVELESQLSSEGSQKASLOKSIKAKIGRCETEE 120
Qy      121 TRLAKELSLRDQREOLKAEVEKYKDCDPQVVEIRQANKVAKKANRWTDNIFAIKSWA 180
Db      121 TRLAKELSLRDQREOLKAEVEKYKDCDPQVVEIRQANKVAKKANRWTDNIFAIKSWA 180
Qy      181 KRKGFEEKNIDRTFGIPEDFDYID 205
Db      181 KRKGFEEKNIDRTFGIPEDFDYID 205

```

```

RESULT 8
US-10-408-765A-1821
; Sequence 1821, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Boia D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Wainock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408.765A
; SOFTWARE: FastSeq for Windows Version 4.0
; NUMBER OF SEQ ID NOS: 3077
; SEQ ID NO 1821
; LENGTH: 205
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-1821

```

```

Query Match
Best Local Similarity 100.0%; Score 1047; DB 16; Length 205;
Matches 205; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      1 MSKKKGLSAEKKRTMEIFSETKDVOLKDLKIAKREKGTMSVKEVLSIVDDGMV 60
Db      1 MSKKKGLSAEKKRTMEIFSETKDVOLKDLKIAKREKGTMSVKEVLSIVDDGMV 60
Qy      61 DCRIGTSNYWAFPSKALHARKHKLVELESQLSSEGSQKASLOKSIKAKIGRCETEE 120
Db      61 DCRIGTSNYWAFPSKALHARKHKLVELESQLSSEGSQKASLOKSIKAKIGRCETEE 120
Qy      121 TRLAKELSLRDQREOLKAEVEKYKDCDPQVVEIRQANKVAKKANRWTDNIFAIKSWA 180
Db      121 TRLAKELSLRDQREOLKAEVEKYKDCDPQVVEIRQANKVAKKANRWTDNIFAIKSWA 180
Qy      181 KRKGFEEKNIDRTFGIPEDFDYID 205
Db      181 KRKGFEEKNIDRTFGIPEDFDYID 205

```

```

RESULT 9
US-10-087-190-44
; Sequence 44, Application US/10087190
; Publication No. US2003022397A1
; GENERAL INFORMATION:
; APPLICANT: Agensys, Inc.
; APPLICANT: Challita-Eld, Pia M.
; APPLICANT: Hubert, Rene S.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Afari, Daniel E. H.
; APPLICANT: Ge, Wangmao
; APPLICANT: Jakobovitz, Aya
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
; ENTITLED 121P1 USEFUL IN TREATMENT AND DETECTION OF CANCER

```

```

; FILE REFERENCE: 51158-20034.20
; CURRENT APPLICATION NUMBER: US/10/087.190
; PRIOR FILING DATE: 2003-01-28
; PRIOR FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-087-190-44

```

```

Query Match
Best Local Similarity 99.0%; Score 1036.5; DB 15; Length 206;
Matches 205; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
Qy      1 MSKKKGLSAEKKRTMEIFSETKDVOLKDLKIAKREKGTMSVKEVLSIVDDGMV 60
Db      1 MSKKKGLSAEKKRTMEIFSETKDVOLKDLKIAKREKGTMSVKEVLSIVDDGMV 60
Qy      61 DCRIGTSNYWAFPSKALHARKHKLVELESQLSSEGSQKASLOKSIKAKIGRCETEE 119
Db      61 DCRIGTSNYWAFPSKALHARKHKLVELESQLSSEGSQKASLOKSIKAKIGRCETEE 119
Qy      120 RTRAKELSLRDQREOLKAEVEKYKDCDPQVVEIRQANKVAKKANRWTDNIFAIKSWA 179
Db      121 TRLAKELSLRDQREOLKAEVEKYKDCDPQVVEIRQANKVAKKANRWTDNIFAIKSWA 180
Qy      180 AKRKGFEENKIDRTFGIPEDFDYID 205
Db      181 AKRKGFEENKIDRTFGIPEDFDYID 206

```

```

RESULT 10
US-10-087-190-45
; Sequence 45, Application US/10087190
; Publication No. US2003022397A1
; GENERAL INFORMATION:
; APPLICANT: Agensys, Inc.
; APPLICANT: Challita-Eld, Pia M.
; APPLICANT: Hubert, Rene S.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Afari, Daniel E. H.
; APPLICANT: Ge, Wangmao
; APPLICANT: Jakobovitz, Aya
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
; FILE REFERENCE: 51158-20034.20
; CURRENT APPLICATION NUMBER: US/10/087.190
; PRIOR FILING DATE: 2003-01-28
; PRIOR FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 45
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-087-190-45

```

```

Query Match
Best Local Similarity 99.0%; Score 1036.5; DB 15; Length 206;
Matches 205; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
Qy      1 MSKKKGLSAEKKRTMEIFSETKDVOLKDLKIAKREKGTMSVKEVLSIVDDGMV 60
Db      1 MSKKKGLSAEKKRTMEIFSETKDVOLKDLKIAKREKGTMSVKEVLSIVDDGMV 60
Qy      61 DCRIGTSNYWAFPSKALHARKHKLVELESQLSSEGSQKASLOKSIKAKIGRCETEE 119
Db      61 DCRIGTSNYWAFPSKALHARKHKLVELESQLSSEGSQKASLOKSIKAKIGRCETEE 120

```

Qy 120 RTRLAKEISLRDREOLKAWEKYKDCDPQVVEIRQANKVAKAANRWTDNIFAIKSM 179
| | | | |
Db 121 RTRLAKEISLRDREOLKAWEKYKDCDPQVVEIRQANKVAKAANRWTDNIFAIKSM 180
| | | | |
Qy 180 AKRKFGEENKIDRTFGIPEDFYID 205
| | | | |
Db 181 AKRKFGEENKIDRTFGIPEDFYID 206
| | | | |

RESULT 11

US-10-087-190-24
; Sequence 24, Application US/10087190
; Publication No. US20030223997A1
; GENERAL INFORMATION:
; APPLICANT: Agensys, Inc.
; APPLICANT: Challita-Bid, Pia M.
; APPLICANT: Hubert, Rene S.
; APPLICANT: Raltano, Arthur B.
; APPLICANT: Farris, Mary
; APPLICANT: Afar, Daniel E. H.
; APPLICANT: Ge, Wangmao

; APPLICANT: Jakobovitz, Aya
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
; TITLE OF INVENTION: ENTITLED 121P1P1 USEFUL IN TREATMENT AND DETECTION OF CANCER
; FILE REFERENCE: 51158-20034.20
; CURRENT APPLICATION NUMBER: US/10/087,190
; CURRENT FILING DATE: 2003-01-28
; PRIOR FILING DATE: 2003-01-28
; PRIOR FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 198
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-087-190-24

Query Match 96.6%; Score 1011; DB 15; Length 198;
Best Local Similarity 100.0%; Pred. No. 2.7e-75;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KGLSAEKRRTMMEIFSETKDVFOLEKIAPEKGIITAMSVKVEYLOSLVDGWDGDCR 64
| | | | |
Db 1 KGLSAEKRRTMMEIFSETKDVFOLEKIAPEKGIITAMSVKVEYLOSLVDGWDGDCR 60
| | | | |
Qy 65 IGTSNYWAFPSKALHARKHKLVEISQISEGSOQKASIQKSIIEKAKIGRCETEERTRIA 124
| | | | |
Db 61 IGTSNYWAFPSKALHARKHKLVEISQISEGSOQKASIQKSIIEKAKIGRCETEERTRIA 120
| | | | |
Qy 125 KELSRLRQREOLKAWEKYKDCDPQVVEIRQANKVAKAANRWTDNIFAIKSM 184
| | | | |
Db 121 KELSRLRQREOLKAWEKYKDCDPQVVEIRQANKVAKAANRWTDNIFAIKSM 180
| | | | |
Qy 185 GFEENKIDRTFGIPEDFYID 202
| | | | |
Db 181 GFEENKIDRTFGIPEDFYID 198
| | | | |

RESULT 12

US-10-087-190-13
; Sequence 13, Application US/10087190
; Publication No. US20030223997A1
; GENERAL INFORMATION:
; APPLICANT: Agensys, Inc.
; APPLICANT: Challita-Bid, Pia M.
; APPLICANT: Hubert, Rene S.
; APPLICANT: Raltano, Arthur B.
; APPLICANT: Farris, Mary
; APPLICANT: Afar, Daniel E. H.
; APPLICANT: Ge, Wangmao
; APPLICANT: Jakobovitz, Aya
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN

US-10-087-190-13

; TITLE OF INVENTION: ENTITLED 121P1P1 USEFUL IN TREATMENT AND DETECTION OF CANCER
; FILE REFERENCE: 51158-20034.20
; CURRENT APPLICATION NUMBER: US/10/087,190
; CURRENT FILING DATE: 2003-01-28
; PRIOR FILING DATE: 2003-01-28
; PRIOR FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 190
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-087-190-13

Query Match 93.1%; Score 975; DB 15; Length 190;
Best Local Similarity 100.0%; Pred. No. 2.3e-72;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 MMEIFSETKDVFOLEKIAPEKGIITAMSVKVEYLOSLVDGWDGDCRIGTSNYWAF 75
| | | | |
Db 1 MMEIFSETKDVFOLEKIAPEKGIITAMSVKVEYLOSLVDGWDGDCRIGTSNYWAF 60
| | | | |
Qy 76 SKALHARKHKLVEISQISEGSOQKASIQKSIIEKAKIGRCETEERTRIA 135
| | | | |
Db 61 SKALHARKHKLVEISQISEGSOQKASIQKSIIEKAKIGRCETEERTRIA 120
| | | | |
Qy 136 OKAWEKYKDCDPQVVEIRQANKVAKAANRWTDNIFAIKSMARKRFGPEENKIDRTF 195
| | | | |
Db 121 OKAWEKYKDCDPQVVEIRQANKVAKAANRWTDNIFAIKSMARKRFGPEENKIDRTF 180
| | | | |
Qy 196 GIPEDFYID 205
| | | | |
Db 181 GIPEDFYID 190
| | | | |

RESULT 13

US-10-087-190-19
; Sequence 19, Application US/10087190
; Publication No. US20030223997A1
; GENERAL INFORMATION:
; APPLICANT: Agensys, Inc.
; APPLICANT: Challita-Bid, Pia M.
; APPLICANT: Hubert, Rene S.
; APPLICANT: Raltano, Arthur B.
; APPLICANT: Farris, Mary
; APPLICANT: Afar, Daniel E. H.
; APPLICANT: Ge, Wangmao
; APPLICANT: Jakobovitz, Aya
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
; TITLE OF INVENTION: ENTITLED 121P1P1 USEFUL IN TREATMENT AND DETECTION OF CANCER
; FILE REFERENCE: 51158-20034.20
; CURRENT APPLICATION NUMBER: US/10/087,190
; CURRENT FILING DATE: 2003-01-28
; PRIOR FILING DATE: 2003-01-28
; PRIOR FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 190
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-087-190-19

Query Match 93.1%; Score 975; DB 15; Length 190;
Best Local Similarity 100.0%; Pred. No. 2.3e-72;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 MMEIFSETKDVFOLEKIAPEKGIITAMSVKVEYLOSLVDGWDGDCRIGTSNYWAF 75
| | | | |
Db 1 MMEIFSETKDVFOLEKIAPEKGIITAMSVKVEYLOSLVDGWDGDCRIGTSNYWAF 60
| | | | |
Qy 76 SKALHARKHKLVEISQISEGSOQKASIQKSIIEKAKIGRCETEERTRIA 135
| | | | |

Db 61 SKALHARKHLEVLSEQLSEGSQKASLOKSIIEKAKIGRCETEERTRLAKELSLRDQRE 120
QY 136 QKAEVEKYKDCDPQVVEIRQANKVAKAANRWTDNIFAIKSWAKRKFGFEENKIDRTF 195
Db 121 QKAEVEKYKDCDPQVVEIRQANKVAKAANRWTDNIFAIKSWAKRKFGFEENKIDRTF 195
QY 196 GIPEDFDYID 205
Db 181 GIPEDFDYID 190

RESULT 14

US-10-087-190-67
; Sequence 67, Application US/10087190
; Publication No. US20030223987A1
; GENERAL INFORMATION:
; APPLICANT: Agensys, Inc.
; APPLICANT: Chailita-Bid, Pia M.
; APPLICANT: Hubert, Rene S.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Fairs, Mary
; APPLICANT: Afar, Daniel E. H.
; APPLICANT: Ge, Wangmao
; APPLICANT: Jakobovitz, Aya
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
; FILE REFERENCE: 51158-20034.20
; CURRENT APPLICATION NUMBER: US/10/087,190
; PRIOR FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: US 09/779,250
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 67
; LENGTH: 190
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-087-190-67

Query Match

Best Local Similarity 93.1%; Score 975; DB 15; Length 190;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 MMEIFSETKDVFOKDKLEKIAPEKEGITTAMSVKEVLOSLVDGMDVCERIGTSNYMAFP 75
Db 1 MMEIFSETKDVFOKDKLEKIAPEKEGITTAMSVKEVLOSLVDGMDVCERIGTSNYMAFP 75
QY 76 SKALHARKHLEVLSEQLSEGSQKASLOKSIIEKAKIGRCETEERTRLAKELSLRDQRE 120
Db 61 SKALHARKHLEVLSEQLSEGSQKASLOKSIIEKAKIGRCETEERTRLAKELSLRDQRE 120
QY 136 QKAEVEKYKDCDPQVVEIRQANKVAKAANRWTDNIFAIKSWAKRKFGFEENKIDRTF 195
Db 121 QKAEVEKYKDCDPQVVEIRQANKVAKAANRWTDNIFAIKSWAKRKFGFEENKIDRTF 195
QY 196 GIPEDFDYID 205
Db 181 GIPEDFDYID 190

RESULT 15

US-10-087-190-68
; Sequence 68, Application US/10087190
; Publication No. US20030223987A1
; GENERAL INFORMATION:
; APPLICANT: Agensys, Inc.
; APPLICANT: Chailita-Bid, Pia M.
; APPLICANT: Hubert, Rene S.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Fairs, Mary
; APPLICANT: Afar, Daniel E. H.
; APPLICANT: Ge, Wangmao
; APPLICANT: Jakobovitz, Aya

; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
; FILE REFERENCE: 51158-20034.20
; CURRENT APPLICATION NUMBER: US/10/087,190
; PRIOR FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: US 09/779,250
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 68
; LENGTH: 190
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-087-190-68

Query Match

Best Local Similarity 93.1%; Score 975; DB 15; Length 190;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 MMEIFSETKDVFOKDKLEKIAPEKEGITTAMSVKEVLOSLVDGMDVCERIGTSNYMAFP 75
Db 1 MMEIFSETKDVFOKDKLEKIAPEKEGITTAMSVKEVLOSLVDGMDVCERIGTSNYMAFP 75
QY 76 SKALHARKHLEVLSEQLSEGSQKASLOKSIIEKAKIGRCETEERTRLAKELSLRDQRE 120
Db 61 SKALHARKHLEVLSEQLSEGSQKASLOKSIIEKAKIGRCETEERTRLAKELSLRDQRE 120
QY 136 QKAEVEKYKDCDPQVVEIRQANKVAKAANRWTDNIFAIKSWAKRKFGFEENKIDRTF 195
Db 121 QKAEVEKYKDCDPQVVEIRQANKVAKAANRWTDNIFAIKSWAKRKFGFEENKIDRTF 195
QY 196 GIPEDFDYID 205
Db 181 GIPEDFDYID 190

Search completed: March 23, 2005, 19:30:49
Job time : 139 secs

A:Residues: 1-128 <BEV>
 A:Cross-references: UNIPROT:O9SZES; EMBL:AL078470; GSPDB:G000062; ATSP:F19B15.200
 A:Experimental source: cultivar Columbia; BAC clone F19B15
 A:Gene: ATRP:F19B15.200
 A:Map position: 4
 A:introns: 13/3; 52/3; 88/3; 109/3

Query Match

Best Local Similarity 18.8%; Score 197; DB 2; Length 128;
 Matches 49; Conservative 23; Mismatches 37; Indels 14; Gaps 3;
 QY 16 MEISETYDVFQKLDLKIAPKRGITAMSVKVLQSLVDGMDCEKIGTSNYWAF 75
 DB 1 MLIETESQDFELKELEKMPK-KGVISQSVADVQLVDDVADKIGIS----- 52
 QY 76 STALHARKLEVESQSLSGQKHAQLQKSEKAKICRGTERTRLAKELSLDQRE 135
 DB 53 --LRSVQK--LESIDLQSNKRLAEVLVDQCALKKGRSEERTALTKLDIEKHK 106
 QY 136 QLK 138
 DB 107 DLK 109

RESULT 3

S61134
 N:Altemate names: hypothetical protein YGL183c - Yeast (Saccharomyces cerevisiae)
 C:Species: Saccharomyces cerevisiae
 C>Date: 23-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 09-Jul-2004
 C/Accession: S61134; S64200
 R:Berant, I.; Cogillevina, M.; Zaccaria, P.; Klima, R.; Brusch, C.V.
 submitted to the EMBL Data Library, September 1995.
 A:Description: The sequence analysis of a 7.9 kb DNA fragment from the left arm of S.cer
 iva new genes.
 A:Reference number: S61128
 A:Accession: S61134
 A:Molecule type: DNA
 A:Residues: 1-174 <BER>
 R:Brusch, C.V.; Cogillevina, M.; Berant, I.; Klima, R.; Zaccaria, P.; Delneri, D.
 submitted to the Protein Sequence Database, May 1996
 A:Accession: S64183
 A:Molecule type: DNA
 A:Residues: 1-174 <BRU>
 A:Cross-references: EMBL:Z72705; NID:G1322796; PID:CA96895.1; PID:e243495; PID:G132279
 C:Experimental source: strain S288C
 A:Gene: SGD:MND1
 A:Cross-references: SGD:S0003151
 A:Map position: 7L

Query Match

Best Local Similarity 16.1%; Score 168.5; DB 2; Length 174;
 Matches 46; Conservative 42; Mismatches 68; Indels 13; Gaps 5;
 QY 45 MSVEVLQSLVD-DGAVDERIGTSNYWAFPSKALHARKLEVESQSLSGQKHA 103
 DB 1 MIVYDVLQWIDEDVIVSEKGNINITYWCFKQGTLOKYSDESEIKIKIDEVKCDIATY 60
 QY 104 QXIERA-KIGCEETERTRLAKELSLRDQREQLAEVEKXKDDPOVEIR----- 156
 DB 61 KQELDKTALATGRKKKFTVQGSYNREALLKRRKQIDETKK-KNSIQKIESIRMAAKI 119
 QY 157 QANK-----VAKAANRTDNIIPAIKSMARKGFEENKIDRTFGIPDF 201
 DB 120 QENQOIRLKKVHLKETTNIILIDYLYKKFKPEQIRREIGIIEEP 168

RESULT 4

JCS368

dynactin 1 - mouse
 N:Altemate names: p150 Glued
 C:Species: Mus musculus (house mouse)
 C/Accession: JCS368
 C/Date: 28-May-1997 #sequence_revision 18-Jul-1997 #text_change 09-Jul-2004
 R:Jiang, W.; Weber, U.S.; Tokito, M.K.; Holzbaur, E.L.F.; Meister, M.H.
 Biochem. Biophys. Res. Commun. 231, 344-347, 1997
 A:Title: Mouse p150Glued (dynactin 1) cDNA sequence and evaluation as a candidate f
 A:Reference number: JCS368; MUID:97223454; PMID:9070275
 A:Accession: JCS368
 A:Molecule type: mRNA
 A:Residues: 1-1281 <JAN>
 A:Cross-references: UNIPROT:O08788; GB:U60312; NID:G2104494; PID:AA57773.1; PID:g2
 A:Experimental source: brain
 C:Comment: This protein is a member of the oligomeric dynactin complex that is requ
 A:Gene: Dcn1
 A:Map position: 6

Query Match

Best Local Similarity 12.9%; Score 135.5; DB 2; Length 1281;
 Matches 50; Conservative 43; Mismatches 106; Indels 15; Gaps 5;
 QY 2 SKKGLSAEKRTRMEIFSEKTVDFQKDLKIAPEKGITAMSVKVLQSLVDGMD 61
 DB 219 ARKAKALBAKRYEMWADTADIEAVATLDKEMAEKESLQDEVEALKERVDLTDD 338
 QY 62 CERL-----GTSNYWAFPSKALHAR-KHKLEVESQSLSGQKHAQLQKSEK 110
 DB 339 LEIKARIEKSDAASSYQLKQLEBQNRKLDALVRRLDSSSEKQEHVKQKMEK- 397
 QY 111 KICRGT--ERTRLAKELSLRDQREQLAEVEKXKDDPOVEIRQANKAKAANR 168
 DB 398 KQELFVVRQQRERLOEELSOAESTIDELKEQVDALGAE-EMVEMLTDRNLLEKRYE 456
 QY 169 WTDNIFAIKSWAKKGFPEENKIDRTFGIPDF 202
 DB 457 LRETVGLLEAMNEMNDXLOENARRELELRDOLD 490

RESULT 5

A41642
 N:Altemate names: chicken
 C:Species: Gallus gallus (chicken)
 C/Accession: A41642
 C/Date: 28-Aug-1992 #sequence_revision 28-Aug-1992 #text_change 09-Jul-2004
 R:Gill, S.R.; Schroer, T.A.; Szilak, I.; Steiner, E.R.; Sheetz, M.P.; Cleveland, D.W.
 J. Cell Biol. 115, 1639-1650, 1991
 A:Title: Dynactin, a conserved, ubiquitously expressed component of an activator of vesic
 A:Reference number: A41642; MUID:92098576; PMID:1836789
 A:Accession: A41642
 A:Status: Preliminary
 A:Molecule type: mRNA
 A:Residues: 1-1053 <GIL>
 A:Cross-ref: 1-1053 <GIL>
 C:Keywords: cytoskeleton

Query Match

Best Local Similarity 12.5%; Score 130.5; DB 2; Length 1053;
 Matches 53; Conservative 42; Mismatches 93; Indels 37; Gaps 7;
 QY 2 SKKGLSAEKRTRMEIFSEKTVDFQKDLKIAPEKGITAMSVKVLQSLVDGMD 57
 DB 101 AKKAKALBAKRYEMWADTADIEAVATLDKEMAEKESLQDEVEALKERVDLTDD 160
 QY 58 GMV--DCRIGTSNYWAFPSKALHARKHLE--VLSQSLSGQKHAQLQKSEK 110
 DB 161 LEIKARIEKSDAASSYQLKQLEBQNRKLDALVRRLDSSSEKQEHVKQKMEK 220
 QY 111 KICRGTERTRLAKELSLRDQREQLAEVEKXKDDPOVEIRQANKAKAANR 267
 DB 221 N-----TELESLRQREKLOEVLVQAKETVDELKEQVDALGAEEMVETL 267

QY 158 ANKVAEAAANRWTDNIFAISWAKRRKGFEEENKIDRTFGIPEDFD 202
 DB 268 RNLDLEEKVELEFETVGDLEANNENMDEIQENARETELELREQLD 312

RESULT 6

kinectin 1 - human
 C:Species: Homo sapiens (man)
 C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #ext_change 09-Jul-2004
 C:Accession: S33763; 137947
 R:Kruppa, G.; Puetterer, A.; Lemke, H.; Kronke, M.
 submitted to the EMBL Data Library, April 1993
 A:Description: Cloning and characterization of TAF, a novel transactivating protein.
 A:Reference number: S33763
 A:Accession: S33763
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-1356 <KRU>
 A:Cross-references: UNIPROT:Q86D2; EMBL:222551
 R:Putterer, A.; Kruppa, G.; Kramer, B.; Lemke, H.; Kronke, M.
 Mol. Biol. Cell 6, 161-170, 1995
 A:Title: Molecular cloning and characterization of human kinectin.
 A:Reference number: 137947; MUID:95306853; PMID:7787243
 A:Accession: 137947
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-1356 <RES>
 A:Cross-references: EMBL:222551; NID:g296163; PIDN:CAA80271.1; PID:g296164
 C:Genetics:
 A:Gene: GDB: KTN1
 A:Cross-references: GDB:6165852; OMIM:600653

Query Match 11.6%; Score 121.5; DB 2; Length 1356;
 Best Local Similarity 22.7%; Pred. No. 2.3;
 Matches 50; Conservative 31; Mismatches 88; Indels 51; Gaps 5;

QY 3 KKKGLSAEKKTRMEIFSETKDVFPOLKLEKIAPEKKGITA--MSKVEVLQSLVDGKV 60
 DB 1025 RKNNDLRKKNWEALASTERKMDKKNKSKKQVQVEALEAKVLLKLPKAV 1084
 QY 61 DCEKIGTSNYWAPPSKALH---ARKKLEVLSEQLSEGSQKASLQKSIKAKIGRC 115
 DB 1085 P-SNLSYCGWHLGFEKKAKCMAAGTSGSEVKVLEHKLKADBMHTLLQLECKKYGVLA 1143
 QY 116 ETE-----BRTFLA-KELSLTD 132
 DB 1144 ETEGILQKLSRVEQENKVKVDESHTIKQMOSSFTSSQELERLSKNKDIENLR 1203
 QY 133 QREQLKAEVKYKDCDPQVVEIRQANKVAEAAANRWTDN 172
 DB 1204 EREHLEMELEKAMERSTYTVRELRKDLTLTSLQKLDLDS 1243

RESULT 7
 T02572
 hypochetrical protein At2g39300 [imported] - Arabidopsis thaliana

N:Alternate names: hypochetrical protein T16B24.6
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #ext_change 09-Jul-2004
 C:Accession: T02572; F84815
 R:Roundley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes,
 submitted to the EMBL Data Library, August 1998
 A:Description: Arabidopsis thaliana chromosome II BAC T16B24 genomic sequence.
 A:Reference number: Z14679
 A:Accession: T02572
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-768 <ROU>
 A:Cross-references: UNIPROT:Q80951; EMBL:AC004697; NID:g3402671; PID:g3402677
 A:Experimental source: cultivar Columbia
 R:Lin, X.; Kaul, S.; Roundley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L.

eus, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Frazer, C.M.; Venter, J
 Nature 402, 761-768, 1999
 A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A:Reference number: A84420; MUID:20083487; PMID:1061197
 A:Accession: F84815
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-768 <STO>
 A:Cross-references: GB:AE002093; NID:g3402671; PIDN:AAC28980.1; GSPDB:GN00139
 C:Genetics:
 A:Gene: T16B24.6; At2g39300
 A:Map position: 2
 A:Introns: 80/2; 665/3

Query Match 11.2%; Score 117; DB 2; Length 768;
 Best Local Similarity 22.1%; Pred. No. 2.5;
 Matches 50; Conservative 46; Mismatches 90; Indels 40; Gaps 9;

QY 1 MSKKGLSAE-----EKTRMEIFSETK-----DVFPOL-KOLEKIAPEKKGIT 43
 DB 247 MCKEDDVSELEKRYKAEKRVKLSSEMEKKFLSDCFDSSIVGDIRQMEERVGL- 305
 QY 44 AMSYKVLQSLVDGMDCEKIGTSNYWAPPSKALHARKHLEVLSEQLSEGSQKAS 102
 DB 306 AFEVLSLRQWDERASTREDIRRVKNPMDLLKLEKEKTELQVLETLDRSSEWTS 365
 QY 103 LQKSIKAKIGRCETREERTLAKELSLRDQEQKAEVEKYKDCDPQVVEIRQANKVA 162
 DB 366 ---KYSEFKV-----EEKRLERVRLEAHNVSLQREISTHEKETERIDMIRHLETV 416
 QY 163 KE---AANRWTDNIFAISWAKRRKGFEEENKIDRTFGIPEDFDYI 204
 DB 417 TELSATAEMERENFLMQLNSKLGESYT-----GSTDLDDYV 454

RESULT 8
 T08621
 centrosome associated protein CEP250 - human

C:Species: Homo sapiens (man)
 C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #ext_change 21-Jul-2000
 C:Accession: T08621
 R:MacK, G.J.; Rees, J.; Sandilow, O.; Balczon, R.; Fritzler, M.J.; Rattner, J.B.
 Arthritis Rheum. 41, 551-558, 1998
 A:Title: Autoantibodies to a group of centrosomal proteins in human autoimmune sera reac
 A:Reference number: Z14662; MUID:98165428; PMID:9506584
 A:Accession: T08621
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-2442 <MAC>
 A:Cross-references: EMBL:AF022655; NID:g2832236; PIDN:AAC06349.1; PID:g2832237
 A:Experimental source: cell line HeLa

Query Match 11.1%; Score 116.5; DB 2; Length 2442;
 Best Local Similarity 19.7%; Pred. No. 9.4;
 Matches 46; Conservative 47; Mismatches 64; Indels 77; Gaps 8;

QY 1 MSKKGLSAEKKTRMEIFSETKDVFPOLKLE--KIAPEKIGTAMSVKVLQSLVDG 58
 DB 1662 LQKRIQVLEDDRTQTKLES-----DLQIKLSRREGRLTTORQMOERAEBSG 1713
 QY 59 M-----VDCR-----RIGTSNYW 72
 DB 1714 KQPSKAGSGLHMKLLIRDKKEVECCQENHHEQLKDLQEQQLGHRVGET---- 1769
 QY 73 AFPSPALHARKHLEVLSEQLSE---GSQKASLQKSIKAKIGRCETERTRIAKELS 128
 DB 1770 ---SLLSQREQEIIVLQQLQEARQCELEKQSLQSLQDEKRALARDQ-----ELE 1820
 QY 129 SLRDQEQKAEVEKYKDCDPQVVEIRQANKVAEAAANRWTDNIFAISWAKR 182
 DB 1821 ALQEQEQQAQGOEERKAKADALQALQALQAHWTLLKERHGELODH---KEQARR 1870

RESULT 9

F75103
 conserved hypothetical protein PAB0812 - Pyrococcus abyssi (strain Orsay)
 C/Species: Pyrococcus abyssi
 C/Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
 C/Accession: F75103
 R/Anonymous: Genoscope
 A/Submitted to the EMBL Data Library, July 1999
 A/Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome structure
 A/Reference number: A75001
 A/Accession: F75103
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-880 <KAM>
 A/Cross-references: UNIPROT:O9U2C8; GB:A248286; GB:AL096836; NID:95458366; PIDN:CA5013
 A/Experimental source: strain Orsay
 C/Genetics:
 A/Name: PAB0812
 C/Superfamily: Archaeoglobus fulgidus conserved hypothetical protein AF1032

Query Match
 Best local similarity 11.0%; Score 115.5; DB 2; Length 880;
 Matches 58; Conservative 38; Mismatches 78; Indels 67; Gaps 10;

QY 3 KKKGL-----SSEKRTMMEIFSETVDVFKDLKPKKGGITAMSVKVLQS 53
 DB 257 RKGLBEKIVQIERSEKKAISLEIVKIDPKQEKERKLGFR----- 306
 QY 54 LVDDGMVDCERTGTSNYWAFPSKAL-----HARKLEVLSEGLSGSKHSL--- 103
 DB 307 --DEYSEKLRLEKELSMSEELKALIEVKEEKKERAEIRELSIEKLEKPY 364
 QY 104 -----QKSIKAK-----IGRCET--EERTLAKELSSL-----RD 132
 DB 365 VEEEDAKOVKQIERKALKLSPEVEIKLESLEKERTIEHAIETTRIGQMEGE 424
 QY 133 QREOLKA--EVEKKKCDPVVEIRQANKVAKAANRWTNIPATSMARKFGEENK 190
 DB 425 KNEEMKAIIEIRKAKKCPVCGELTEBK--KELMEVYTLIEIKIEELKRTTE--EERK 481
 QY 191 I 191
 DB 482 L 482

RESULT 10

S24972
 tropomyosin alpha, cardiac - pig
 C/Species: Sus scrofa domestica (domestic pig)
 C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
 C/Accession: S24972
 R/Whitby, F.G.; Kent, H.M.; Stewart, F.; Stewart, M.; Xie, X.; Hatch, V.; Cohen, C.; Phil
 submitted to the EMBL Data Library, April 1992
 A/Description: Structure of tropomyosin at 9 Angstroms resolution.
 A/Reference number: S24972
 A/Accession: S24972
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-284 <WHI>
 A/Cross-references: UNIPROT:P42639; EMBL:X66274; NID:91926; PIDN:CAA46966.1; PID:91927
 C/Keywords: cardiac muscle; heart

Query Match
 Best local similarity 23.2%; Pred. No. 1.3;
 Matches 52; Conservative 37; Mismatches 61; Indels 74; Gaps 11;

QY 1 MSKKGLSAE---EKTRTMEIFSETVDVFKDLKPKKGGITAMSVKVLQS 57
 DB 73 LAEKATDAEDVASINRRIOLEFEELDRAQ---ERLA-----TALQLEAEKRADE 122
 QY 58 --GMVDCERTGTSNYWAFPSKALHAR---KHLLEVLSEGLSGSKHSL----- 100

DB

123 SERGM-----

-----KVESRAQDEKKEHIOELKKA--KHIAEDARKYE 163

QY

101 -----ASLQKSIKAKI--GRCTEERTRLAKELSSLRDRELQKAEVKYDCD 148

DB

164 EVARKLVIESDLERAEERALESEGC-----AELEBELKVTNNKLSLEAKYQKE 218

QY

149 PQVEEIRQANKVAKAANRWTNIPATSMARKFGEENKID 192

DB

219 KYEEELKIVLSDKLEAEFR-----AEFRKSVTKLEKSID 254

RESULT 11

T05409
 hypothetical protein F10M6.170 - Arabidopsis thaliana
 C/Species: Arabidopsis thaliana (mouse-ear cress)
 C/Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
 R/Bevan, M.; Weichselgartner, M.; Fartmann, B.; Granderath, K.; Dauner, D.; Herzl, A
 submitted to the Protein Sequence Database, February 1998
 A/Reference number: Z15414
 A/Accession: T05409
 A/Molecule type: DNA
 A/Residues: 1-764 <BEV>
 A/Cross-references: UNIPROT:O49371; EMBL:AL021811
 A/Experimental source: cultivar Columbia; BAC clone F10M6
 A/Map position: 4
 A/Note: F10M6.170

Query Match
 Best local similarity 10.9%; Score 114; DB 2; Length 764;
 Matches 42; Conservative 40; Mismatches 78; Indels 24; Gaps 5;

QY 8 SAEKRTMMEIFSETVDVFKDLKPKK-----GITAMSVKVLQS 58
 DB 49 SAESANVLEDKLFAKTHLEKQTHSHVYPDDDLVSNLSVLESDLEALVALKEED 108
 QY 59 MVDCERTGTSNYWAFPSKALHARKHLEVLSEGLSGSKQRIASLQKSIKAKI 118
 DB 109 LHDARKLSD-----KNKLNKAELEKREKTTISEASLVHSEIQLELKRANV--ELA 159
 QY 119 ERTLAKELSLRDRELQKAEVKYDCDQVVEIRQANKVAKAANRWTNIPATSM 178
 DB 160 SQAREIEELGHKLRERDERALQSSLTLEKELEKRYQ-----ELANSKEVSMALSE 213
 QY 179 WAKR 182
 DB 214 FEKK 217

RESULT 12

A32183
 tropomyosin TPM1 - yeast (Saccharomyces cerevisiae)
 N/Alternate names: Protein N2132; Protein YML079C
 C/Species: Saccharomyces cerevisiae
 C/Date: 08-Sep-1989 #sequence_revision 08-Sep-1989 #text_change 09-Jul-2004
 R/Jiu, H.; Breitschger, A.
 Cell 57, 233-242, 1989
 A/Title: Disruption of the single tropomyosin gene in yeast results in the disappearance

A/Reference number: A32183; MID:89195234; PMID:2649250
 A/Accession: A32183
 A/Molecule type: DNA
 A/Residues: 1-199 <LTU>
 A/Cross-references: UNIPROT:P17536; EMBL:M25501; NID:9173037; PIDN:AAA35174.1; PID:91730

submitted to the EMBL Data Library, April 1995
 A/Reference number: S53896
 A/Accession: S53896
 A/Molecule type: DNA
 A/Residues: 1-199 <POB>

A/Cross-references: EMBL:X66470; NID:9791101; PIDN:CAA60179.1; PID:9791105
 R/Boehlmann, R.; Philippen, P.

submitted to the Protein Sequence Database, April 1996
 A:Reference number: S62997
 A:Accession: S63011
 A:Molecule type: DNA
 A:Residues: 1-199 <POW>
 A:Cross-references: EMBL:Z71355; NID:g1301970; PIDN:CAA95953.1; PID:g1301971; MIPS:YNL07
 A:Experimental source: strain S288C
 R:Solier-Mira, A.; Saitz, J.E.; Ballesta, J.P.G.; Remacha, M.
 submitted to the Protein Sequence Database, April 1996
 A:Reference number: S63018
 A:Accession: S63018
 A:Molecule type: DNA
 A:Residues: 1-199 <SOI>
 A:Cross-references: EMBL:Z71355; NID:g1301970; PIDN:CAA95953.1; PID:g1301971; MIPS:YNL07
 A:Experimental source: strain S288C
 R:Poehlmann, R.; Philippsen, P.
 Yeast 12, 301-402, 1996
 A:Title: Sequencing a cosmid clone of *Saccharomyces cerevisiae* chromosome XIV reveals 12
 A:Reference number: S63925; MUID:96267764; PMID:8701611
 A:Accession: S63928
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-199 <POF>
 A:Cross-references: EMBL:X86470; NID:g791101; PIDN:CAA60179.1; PID:g791105
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, April 1995
 C:Genetics:
 A:Gene: SGD:TPM1
 A:Cross-references: SGD:S0005023; MIPS:YNL079C
 A:Map position: 14L
 C:Superfamily: tropomyosin TPM1
 C:Keywords: coiled coil; cytoskeleton

Query Match 10.8%; Score 113; DB 2; Length 199;
 Best Local Similarity 24.7%; Pred. No. 1;
 Matches 46; Conservative 40; Mismatches 54; Indels 46; Gaps 8;
 QY 7 LSAERTRRMIEFSETKDVPQLKLEKAPKEGTTASVEVLQSLVDD-----GMV 60
 DB 13 LEAEWQKEVELEKKNQDLQ-ENVE-----KENQKSLTVN--QQLDELEKLEAGUS 65
 QY 61 DCRIGTSNYVWAFPSKALHARKHL-----EVLQSLSG-----SGK 99
 DB 66 DSKQKQEDVKEKQKSLTVNQHLEBEIEKLEAEALSKQSLSDSHHLSNNDFSK 125
 QY 100 HASLQKSLFKAKIGCETFEETRR-----LAKELSLRDQREQKAVE---KYKCC 147
 DB 126 NQOLEDELESDTKLKETTEKLESDLKADQLERRVALEQREWERKNEELTVYCYEDA 185
 QY 148 DPQVVE 153
 DB 186 KKELE 191

RESULT 13
 JG6199
 alpha-tropomyosin S-1 - axolotl
 C:Species: Ambystoma mexicanum (axolotl)
 C:Date: 11-Apr-1997 #sequence_revision 09-May-1997 #text_change 09-Jul-2004
 C:Accession: JG6199
 R:Luque, E.A.; Spinner, B.J.; Dube, S.; Dube, D.K.; Lemanski, L.F.
 Gene 185, 175-180, 1997
 A:Title: Differential expression of a novel isoform of alpha-tropomyosin in cardiac and
 A:Reference number: JG6198; MUID:97208870; PMID:9055812
 A:Contents: skeletal muscle
 A:Accession: JG6199
 A:Molecule type: mRNA
 A:Residues: 1-284 <LUQ>
 A:Cross-references: UNIPROT:P87349; GB:U33450; NID:g1871357; PIDN:AA60092.1; PID:g18713
 C:Comment: This protein is a actin-binding protein.
 C:Genetics:
 A:Gene: Atms-1
 C:Superfamily: tropomyosin
 C:Keywords: actin binding

Query Match 10.7%; Score 112; DB 2; Length 284;
 Best Local Similarity 22.7%; Pred. No. 1.8;
 Matches 48; Conservative 41; Mismatches 74; Indels 48; Gaps 9;
 QY 1 MSKKGLSNEF---KRTMMEIFSETKVFO-----LKDLKAPK-EKGTANSV 47
 DB 73 LARKKATPAESDVASINRIQLVEBELRAERLATALQKEAEKADDESBRGMKVIEN 132
 QY 48 KEVLSLVDDGVDCERIGTSNYVWAFPSKALHARKHLEVLQSLSGSQK---HASL 103
 DB 133 R---ALQDEKMELOEI-----QLQEKHIAEADRYEEVARKLVITIGDL 176
 QY 104 QKSIKAKI--GRCTEERTRLAKELSLRDQREQLKAEVYKDCDPQVEIRQANKV 161
 DB 177 ERAERARLSECKC-----AELEELKTVTNLKLAEQAKEYSQKEDKYEEIRVLTDK 231
 QY 162 AKKANRWTDNIFAIKSWAKRKFGEENKID 192
 DB 232 LKEETR-----AFPAERTVAKLEKSID 254

RESULT 14
 A24199
 tropomyosin NM, skeletal muscle - human
 C:Species: Homo sapiens (man)
 C:Date: 02-Jun-1998 #sequence_revision 02-Jun-1998 #text_change 13-Aug-1999
 C:Accession: S06210; A24199
 R:Clayton, L.; Reinach, F.C.; Chumbley, G.M.; Macleod, A.R.
 J. Mol. Biol. 201, 507-515, 1988
 A:Title: Organization of the hTm(m) gene. Implications for the evolution of muscle and
 A:Reference number: S02554; MUID:88332987; PMID:3418707
 A:Accession: S06210
 A:Status: not compared with conceptual translation
 A:Molecule type: DNA
 A:Residues: 1-285 <CLA>
 R:Reinach, F.C.; Macleod, A.R.
 Nature 332, 648-650, 1986
 A:Title: Tissue-specific expression of the human tropomyosin gene involved in the genera
 A:Reference number: A24199; MUID:8631274; PMID:3018581
 A:Accession: A24199
 A:Molecule type: mRNA
 A:Residues: 1-285 <REI>
 A:Cross-references: GB:X04201; NID:g37429; PIDN:CAA27798.1; PID:g37430
 A:Note: an intronless pseudogene resembling this mRNA is also known
 C:Superfamily: tropomyosin
 C:Keywords: alternative splicing; coiled coil; muscle; skeletal muscle

Query Match 10.7%; Score 112; DB 2; Length 285;
 Best Local Similarity 23.5%; Pred. No. 1.8;
 Matches 52; Conservative 41; Mismatches 72; Indels 56; Gaps 9;
 QY 1 MSKKGLSNEF---KRTMMEIFSETKVFO-----LKDLKAPK-EKGTANSV 47
 DB 74 LAERKAADAEAVASINRIQLVEBELRAERLATALQKEAEKADDESBRGMKVIEN 133
 QY 48 KEVLSLVDDGVDCERIGTSNYVWAFPSKALHARKHLEVLQSLSGSQKHAASLQSKI 107
 DB 134 R---ALQDEKMELOEI-----QLQEKHIAEADRYEEVARKLVITIGDL 177
 QY 108 EKAKIGCTEERTRLA-----KELSLRDQREQLKAEVYKDCDPQVEIRQANKV 159
 DB 178 ER-----TERRALASKECELEELKVTNNLKLAEQAKEYSQKEDKYEEIRKILT 230
 QY 160 KVAKKANRWTDNIFAIKSWAKRKFGEENKIDRTFGIPED 200
 DB 231 DLKKEAETRAE---FAERSVA-----KLEKTIIDLED 259

RESULT 15
 S49143
 Eg10 protein - tapeworm (Echinococcus granulosus)
 C:Species: Echinococcus granulosus

C>Date: 16-Feb-1995 #sequence_revision 12-May-1995 #text_change 15-Mar-2004
 C/Accession: S49143
 R/Frosch, P.M.; Hartmann, M.; Sygulla, L.; Margutti, P.; Frosch, M.
 submitted to the EMBL Data Library, January 1994
 A/Description: Identification of a cDNA clone from the larval stage of *Echinococcus gran*
 A/Reference number: S49143
 A/Accession: S49143
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-559 <PRO>
 A/Cross-references: EMBL:Z29489; NID:9509759; PIDN:CAA82625.1; PID:9509760
 C/Superfamily: ezrin/radixin/moesin; protein 4.1 membrane-binding domain homology
 F:12-293/Domain: protein 4.1 membrane-binding domain homology <B41>

Query Match 10.7%; Score 112; DB 2; Length 559;
 Best Local Similarity 27.8%; Pred. No. 3.7;
 Matches 49; Conservative 34; Mismatches 61; Indels 32; Gaps 7;

QY	1	MSKKKGLSAEERKPTMMELFSETKDVPQLKDLKLAPEKEGTTAMSVKEVLTQSLVDGMY	60
DB	294	MRRRKSDSIYQOMKI-----QAKERELKEAERQLKESRLQRMENEQKLREIRAQ-MW	347
QY	61	DCERIGTSNYWAFPPSKALHARKHLEVLSEQLSE-----GSQKHA--SLQKSLER-AKI	112
DB	348	EKE-----SDLADMKNKASAYESKIALEMLQGERHARESLLQKSQDKLAEM	394
QY	113	GRCEETERTRLAKELSLRQREQLKAVEKYKDCDPQVVEETIRQANKVAKAENR	168
DB	395	NRKAKEETAAEAERNRRLMAQRDEVQREVAOK-----VAMAKKEAKAQAEAEELR	445

Search completed: March 23, 2005, 19:18:39
 Job time : 43 secs

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OM protein - protein search, using SW model

Run on: March 23, 2005, 19:08:01 ; Search time 177 Seconds

(without alignments)
593.086 Million cell updates/sec

Title: US-10-087-190-3

Perfect score: 1047
Sequence: 1 MSKKKGSAEKRTRMEIF.....FEENKIDRTFGIPEDFDYID 205

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1047	100.0	205	Q9BWT6	Q9BWT6 homo sapien
2	954	91.1	205	Q8K396	Q8K396 mus musculi
3	948	90.5	205	Q9D0A1	Q9D0A1 mus musculi
4	644	61.5	220	Q6DC61	Q6DC61 brachydanio
5	462	44.1	196	Q8EEZ8	Q8EEZ8 schistosoma
6	440	42.0	230	Q8GYD2	Q8GYD2 oryza sativ
7	427	40.8	207	Q6H432	Q6H432 oryza sativ
8	349	33.3	210	YAS3 SCHPO	Q89739 schizosacch
9	340.5	32.5	203	Q8SU9	Q8SU9 encephalito
10	340.5	32.5	203	Q6WDA3	Q6WDA3 giardia lam
11	340.5	32.5	203	Q7QTX0	Q7QTX0 giardia lam
12	332.5	31.8	179	Q6Q9F9	Q6Q9F9 aedes aegy
13	277	26.5	196	Q7RH53	Q7RH53 plasmodium
14	266.5	25.5	211	Q6B0L5	Q6B0L5 debaromyce
15	221	21.1	225	Q75CH5	Q75CH5 ashyia goss
16	206.5	19.7	225	Q6CSX5	Q6CSX5 kluyveromyc
17	197	18.8	128	Q9S2B5	Q9S2B5 arabidopsi
18	175	16.7	222	Q6FL56	Q6FL56 candida gla
19	168.5	16.1	174	YGT3 YEAST	YGT3 YEAST
20	153.5	14.7	101	Q6E679	Q6E679 nosema locu
21	136.5	13.0	910	Q7T2F8	Q7T2F8 brachydanio
22	135.5	12.9	1281	Q6AWB1	Q6AWB1 mus musculi
23	134.5	12.8	890	Q6AWB1	Q6AWB1 mus musculi
24	134.5	12.8	890	Q6AWB3	Q6AWB3 homo sapien
25	134.5	12.8	1139	Q6IQ37	Q6IQ37 homo sapien
26	134.5	12.8	1264	Q6NZM3	Q6NZM3 mus musculi
27	134.5	12.8	1278	Q6MZ23	Q6MZ23 homo sapien
28	134.5	12.8	1278	Q6MZ23	Q6MZ23 homo sapien
29	131.5	12.6	1280	DYNA_RAT	DYNA_RAT
30	130.5	12.5	1224	DYNA_CHICK	DYNA_CHICK
31	126.5	12.1	1232	Q6PCJ1	Q6PCJ1 xenopus lae

32	126	12.0	609	2	Q8TXA4	Q8TXA4 mechanopyru
33	122.5	11.7	797	2	Q6GLB3	Q6GLB3 xenopus tro
34	122	11.7	10578	2	Q8ISF5	Q8ISF5 caenorhabdi
35	122	11.7	18519	2	Q8ISF6	Q8ISF6 caenorhabdi
36	122	11.7	18534	2	Q8ISF7	Q8ISF7 caenorhabdi
37	121.5	11.6	995	2	Q6FLN4	Q6FLN4 meoplasma
38	121.5	11.6	1357	1	KTNI_HUMAN	KTNI_HUMAN
39	121.5	11.6	1364	1	KTNI_CHICK	KTNI_CHICK
40	120.5	11.5	172	2	Q824V3	Q824V3 gallus gall
41	120.5	11.5	448	2	Q84H59	Q84H59 anaplasma m
42	120.5	11.5	1732	2	Q9YJ35	Q9YJ35 dirosophila
43	120	11.5	882	1	RA50_PRRU	RA50_PRRU
44	120	11.5	1120	1	ERCI_MOUSE	ERCI_MOUSE
45	118.5	11.3	1177	2	Q87711	Q87711 pyrococcus

ALIGNMENTS

RESULT 1
Q9BWT6 PRELIMINARY; PRT: 205 AA.
ID Q9BWT6; PRT: 205 AA.
AC Q9BWT6; PRT: 205 AA.
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE GAF.
GN Name=GAF;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Solis G., Hofer H.W.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RX MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strusberg R., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein W.J., Usdin T.B., Toshiyuki S., Carrinci P., Prange C.,
RA Raha S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,
RA Krzywinski M.I., Skalski U., Smallos D.E., Scherch A., Schein J.E.,
RA Jones S.J., Maira M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RA Strusberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY028916; AAK26168.1; -;
DR EMBL; BC032142; AAH32142.1; -;
DR InterPro; IPR005647; Mnd1.
DR InterPro; IPR009058; wing_hlx_DNA_bnd.
DR Pfam; PF03962; Mnd1; 1.
SQ SEQUENCE 205 AA; 23753 MW; 95B0B1406BDA0B51 CRC64;
Query Match 100.0%; Score 1047; DB 2; Length 205;

Best Local Similarity 100.0%, Pred. No. 5.9e-56;
Matches 205; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MSKKGSLAEKRTMMEIFSETKDVQOLDEKLAPEKGTITAMSVKEVLOSVDGMV
DB 1 MSKKGSLAEKRTMMEIFSETKDVQOLDEKLAPEKGTITAMSVKEVLOSVDGMV
QY 61 DCERIGTSNYWAPPSFALHARKHLEVESQSLSSQSHASLOKSEIKAKIGRCETEER
DB 61 DCERIGTSNYWAPPSFALHARKHLEVESQSLSSQSHASLOKSEIKAKIGRCETEER
QY 121 TRIAKELSLRDQREOLKAEVEKYKDCDPQVVEEIRQANKYAKKANRWTDNIFALKSMA
DB 121 TRIAKELSLRDQREOLKAEVEKYKDCDPQVVEEIRQANKYAKKANRWTDNIFALKSMA
QY 121 TRIAKELSLRDQREOLKAEVEKYKDCDPQVVEEIRQANKYAKKANRWTDNIFALKSMA
DB 121 TRIAKELSLRDQREOLKAEVEKYKDCDPQVVEEIRQANKYAKKANRWTDNIFALKSMA
QY 181 KRKFGFEENKIDRTFGIPEDFDYID 205
DB 181 KRKFGFEENKIDRTFGIPEDFDYID 205

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RESULT 2

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ID 08K396 PRELIMINARY; PRT; 205 AA.
AC 08K396;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DE 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE GAV protein.
GN Name=2610034E18Rik;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Mammary tumor;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.D., Feingold E.A., Grouse L.H., Derge J.G.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schenker C.M., Schuler G.D.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Martusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
RA Raha S.S., Lounellano N.A., Toshikiyaki S., Carninci P., Franke C.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,
RA Krzyzanski M.I., Skalska U., Smalls D.E., Scherch A., Schein J.E.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Mammary tumor;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Komno H., Akizawa J., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Suni N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A.,
RA Yamamoto R., Matsunoto H., Sakaguchi S., Ikegami T., Kaishiwagi K.,
RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Matshiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
RT "RIKEN integrated sequence analysis (RISA) system-384-format

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DB 1 MSKKGSLAEKRTMMEIFSETKDVQOLDEKLAPEKGTITAMSVKEVLOSVDGMV
QY 61 DCERIGTSNYWAPPSFALHARKHLEVESQSLSSQSHASLOKSEIKAKIGRCETEER
DB 61 DCERIGTSNYWAPPSFALHARKHLEVESQSLSSQSHASLOKSEIKAKIGRCETEER
QY 121 TRIAKELSLRDQREOLKAEVEKYKDCDPQVVEEIRQANKYAKKANRWTDNIFALKSMA
DB 121 TRIAKELSLRDQREOLKAEVEKYKDCDPQVVEEIRQANKYAKKANRWTDNIFALKSMA
QY 121 TRIAKELSLRDQREOLKAEVEKYKDCDPQVVEEIRQANKYAKKANRWTDNIFALKSMA
DB 121 TRIAKELSLRDQREOLKAEVEKYKDCDPQVVEEIRQANKYAKKANRWTDNIFALKSMA
QY 181 KRKFGFEENKIDRTFGIPEDFDYID 205
DB 181 KRKFGFEENKIDRTFGIPEDFDYID 205

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RESULT 3

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ID 09D0A1 PRELIMINARY; PRT; 205 AA.
AC 09D0A1;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DE 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Mus musculus 10 days embryo whole body cDNA, RIKEN full-length
DE enriched library, clone:2610034E18 product:GAV homolog.
GN Name=2610034E18Rik;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.,
RT "High efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RA The FANTOM Consortium;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Komno H., Akizawa J., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Suni N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A.,
RA Yamamoto R., Matsunoto H., Sakaguchi S., Ikegami T., Kaishiwagi K.,
RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Matshiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
RT "RIKEN integrated sequence analysis (RISA) system-384-format

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RT sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=whole body;
 RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
 RA Arakawa T., Bono H., Carininci P., Fukuda S., Fukunishi Y., Furuno M.,
 RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hirooka T., Horii F.,
 RA Imocani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
 RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
 RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
 RA Okaaki Y., Okido T., Owa C., Saio R., Saio R., Sakai C., Sakai K.,
 RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
 RA Sogabe Y., Suzuki H., Tagami T., Tagawa A., Takahashi F., Tanaka T.,
 RA Teijima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
 RA Muramatsu M., Hayashizaki Y.;
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK011664; BAB27765.1; -;
 DR MGI; MGI:1924165; 2610034E18R1k.
 DR InterPro; IPR005647; Mnd1.
 DR Pfam; PF03962; Mnd1; 1.
 SQ SEQUENCE 205 AA; 23909 MW; 09368E19EA224021 CRC64;
 Query Match 90.5%; Score 948; DB 2; Length 205;
 Best Local Similarity 89.3%; Pred. No. 5,6e-50;
 Matches 183; Conservative 10; Mismatches 12; Indels 0; Gaps 0;
 QY 1 MSKKGSLAEKRTMMEIFSETKDVFOKLEKIAPEKGTAMSVKEVLSVDDGV 60
 DB 1 MSKKGSLAEKRTMMEIFSETKDVFOKLEKIAPEKGTAMSVKEVLSVDDGV 60
 QY 61 DCEKIGTSNYVAFPSKALHARKHLEKLEVSQSGQKASLOKSEKAKIGRCETTER 120
 DB 61 DCEKIGTSNYVAFPSKALHARKHLEKLEVSQSGQKASLOKSEKAKIGRCETTER 120
 QY 121 TRLAEKSLRQREQLKAEVEKYDCDPQVVEIRQANKVAKAANRWTDNIFAIKSWA 180
 DB 121 AMLAKELSFQDFQOLKAEVEKYDCDPQVVEIRQANKVAKAANRWTDNIFAIKSWA 180
 QY 181 KRKGFENKIDRTFGIPEDFYID 205
 DB 181 KRKGFENKIDRTFGIPEDFYID 205
 DB 181 KRKGFENKIDRTFGIPEDFYID 205
 RESULT 4
 QY 06DC61 PRELIMINARY; PRT; 220 AA.
 AC 06DC61;
 DT 25-OCT-2004 (TREMBLrel. 28, Created)
 DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
 DE Zgc101017 protein.
 GN Name=zgc101017;
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OC NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Singapore local strain; TISSUE=Embryo;
 RX PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schaller G.D.,
 RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stalcenon M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.S.,
 RA Raha S.S., Loguigliano N.A., Peters G.J., Abramson R.D., Mallary S.J.,
 RA Bosh S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalsoud U., Smalls D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Maitra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [12]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Singapore local strain; TISSUE=Embryo;
 RC Director MGC Project;
 RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC078223; AAH78223.1; -;
 DR InterPro; IPR005647; Mnd1.
 DR InterPro; IPR009058; Wing_hlx_DNA_bnd.
 DR Pfam; PF03962; Mnd1; 1.
 SQ SEQUENCE 220 AA; 25176 MW; 90DEAA69311F4BF7 CRC64;
 Query Match 61.5%; Score 644; DB 2; Length 220;
 Best Local Similarity 71.8%; Pred. No. 1.4e-31;
 Matches 125; Conservative 20; Mismatches 29; Indels 0; Gaps 0;
 QY 1 MSKKGSLAEKRTMMEIFSETKDVFOKLEKIAPEKGTAMSVKEVLSVDDGV 60
 DB 1 MSKKGSLAEKRTMMEIFSETKDVFOKLEKIAPEKGTAMSVKEVLSVDDGV 60
 QY 61 DCEKIGTSNYVAFPSKALHARKHLEKLEVSQSGQKASLOKSEKAKIGRCETTER 120
 DB 61 DCEKIGTSNYVAFPSKALHARKHLEKLEVSQSGQKASLOKSEKAKIGRCETTER 120
 QY 121 TRLAEKSLRQREQLKAEVEKYDCDPQVVEIRQANKVAKAANRWTDNIFAIKSWA 174
 DB 121 EDLKLKLTALKGQDKQKVEIKYDCDPQVVEIRQANKVAKAANRWTDNIFAIKSWA 174
 DB 121 EDLKLKLTALKGQDKQKVEIKYDCDPQVVEIRQANKVAKAANRWTDNIFAIKSWA 174
 RESULT 5
 QY 086E28 PRELIMINARY; PRT; 196 AA.
 AC 086E28;
 DT 01-JUN-2003 (TREMBLrel. 24, Created)
 DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Clone ZGD1259 mRNA sequence.
 OS Schistosoma japonicum (blood fluke).
 OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeididae;
 OC Schistosomatoidea; Schistosomatidae; Schistosoma.
 OC NCBI_TaxID=6182;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22879925; PubMed=12973349; DOI=10.1038/ng1236;
 RA Hu W., Yan Q., Shen D.K., Liu F., Zhu Z.D., Song H.D., Xu X.R.,
 RA Wang Z.J., Rong Y.P., Zeng L.C., Wu J., Zhang X., Wang J.Q., Xu X.N.,
 RA Wang S.Y., Fu G., Zhang X.L., Wang Z.Q., Brindley P.J., McManus D.P.,
 RA Xue C.L., Feng Z., Chen Z., Han Z.G.;
 RT "Evolutionary and biomedical implications of a Schistosoma japonicum
 RT complementary DNA resource";
 RL Nat. Genet. 35:139-147(2003).
 DR EMBL; AY223066; AAP06089.1; -;
 DR InterPro; IPR005647; Mnd1.
 DR Pfam; PF03962; Mnd1; 1.
 SQ SEQUENCE 196 AA; 23163 MW; B30P6F08B07123F0 CRC64;
 Query Match 44.1%; Score 462; DB 2; Length 196;
 Best Local Similarity 47.4%; Pred. No. 1.2e-20;
 Matches 92; Conservative 34; Mismatches 68; Indels 0; Gaps 0;
 QY 11 EKRTMMEIFSETKDVFOKLEKIAPEKGTAMSVKEVLSVDDGVDCERIGTSNY 70
 DB 2 KSRQRMDDFFKQPFQKLEKLEKQKESKINSVKQVLSVDDGVLDKIGTSNY 61
 QY 71 YVAFPSKALHARKHLEKLEVSQSGQKASLOKSEKAKIGRCETTERTRIAKELSSL 130

Db 62 FMAFPSKAAQKRNRIEKTGDIHTNRQIFKTRTSINEALSKRKOTEEENKINILTEL 121
 QY 131 RDQREQLKAEVEKYKDCDPQVEEIRQANKVAEANKRWTDNI FALKSNAPKRGFEENK 190
 Db 122 KILBELTLELQDEKHDHDBRLSEIRQOOLVADSNARKWTDNIFALKSNLNSKFLDEAT 181
 QY 191 IIRTGIPEDPDYI 204
 Db 182 FCRQEIPEPDYI 195

RESULT 6

Q8GYD2 PRELIMINARY; PRT; 230 AA.
 ID Q8GYD2
 AC 08GYD2
 DT 01-MAR-2003 (Tremblrel. 23, Created)
 DT 05-JUL-2004 (Tremblrel. 23, Last sequence update)
 DE Hypothetical protein At4g29170/F19B15_200 (Hypothetical protein
 DE At4g29170).
 GN Name=At4g29170/F19B15_200; Synonyms=At4g29170;
 OS Arabidopsis thaliana (mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC Eucaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC NCBI_TaxId=3702; Brasicales; Brassicaceae; Arabidopsis.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Seki M., Iida K., Satou M., Sakurai T., Akiyama K., Ishida J.,
 RA Nakajima M., Enju A., Kamiya A., Natusaka M., Carninci P., Kawai J.,
 RA Hayashizaki Y., Shinozaki K.,
 RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Yamada K., Chan M.M., Chang C.H., Dale J.M., Heuan V.W., Lee J.M.,
 RA Onodera C.S., Quach H.L., Tang C., Toriumi M., Wong C., Wu H.C.,
 RA Yu G., Yuan S., Carninci P., Chen H., Cheuk R., Hayashizaki Y.,
 RA Ishida J., Jones T., Kamiya A., Kawai J., Kim C.U., Natusaka M.,
 RA Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shinn P.,
 RA Southgate A., Trupp M.G., Wu T., Shinozaki K., Davis R.W., Ecker J.R.,
 RA Theologis A.,
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK117113; BAC42364.1;
 DR EMBL; BT005435; AAO63855.1;
 DR InterPro: IPR005639; endotoxin_N.
 DR InterPro: IPR005647; Mnd1.
 DR Pfam: PF03962; Mnd1; 1.
 DR KW Hypothetical protein.
 SQ SEQUENCE 230 AA; 26402 MW; 131BBS146D8C91ED CRC64;

Query Match 42.0%; Score 440; DB 2; Length 230;
 Best Local Similarity 43.8%; Pred. No. 3.2e-19;
 Matches 91; Conservative 43; Mismatches 70; Indels 4; Gaps 2;

QY 1 MSKKKGSAEKKTRMEIFSETKQVFOFKDLKIAPEKKITMSYKVLQSLVDDGWY 60
 Db 1 MSKKKGSLSEKKERKMLQIFYSQDFLLKELKKGPR-KGVISQSVKVDYIQLVDDIV 59
 QY 61 DCRIGTSNYVAFPKALHARKHLEVLSESGSQKASLOKSIKXIGRCCTER 120
 Db 60 ANDKIGISIFWSPSCAGNQLRSVRQKLESDDLQSGNKRILAEVLDCGLAKKGRSESEER 119
 QY 121 TRLAKELSLRQKQLAEVEKYKDCDPQVEEIRQANKVAEANKRWTDNIFALKSMA 180
 Db 120 TRLAKELSLRQKQLAEVEKYKDCDPQVEEIRQANKVAEANKRWTDNIFALKSMA 180
 QY 181 KRKGFEEENKIDRTF--GIPEPDYID 205
 Db 180 SNNFPQAKELHLYTAGITEDPDYIE 207

RESULT 7

Q6H432 PRELIMINARY; PRT; 207 AA.
 ID Q6H432
 AC Q6H432
 DT 05-JUL-2004 (Tremblrel. 27, Created)
 DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
 DE Putative GAI protein.
 GN Name=P0651G05.20;
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Eucaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC NCBI_TaxId=39947; Oryzae; Oryza.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Sasaki T., Matsumoto T., Katayose Y.,
 RA "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 9, PAC
 RT clone:P0651G05.2";
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AP006528; BAD26517.1;
 DR InterPro: IPR005647; Mnd1.
 DR Pfam: PF03962; Mnd1; 1.
 SQ SEQUENCE 207 AA; 23900 MW; 6A9C5ECBEB6D586E CRC64;

Query Match 40.8%; Score 427; DB 2; Length 207;
 Best Local Similarity 42.5%; Pred. No. 1.7e-18;
 Matches 88; Conservative 44; Mismatches 71; Indels 4; Gaps 2;

QY 1 MSKKKGSAEKKTRMEIFSETKQVFOFKDLKIAPEKKITMSYKVLQSLVDDGWY 60
 Db 1 MSKKKGSLSEKKERKMLQIFYSQDFLLKELKKGPR-KGVISQSVKVDYIQLVDDIV 59
 QY 61 DCRIGTSNYVAFPKALHARKHLEVLSESGSQKASLOKSIKXIGRCCTER 120
 Db 60 IKDKIGTSYVFWSPSCAGNQLRSVRQKLESDDLQSGNKRILAEVLDCGLAKKGRSESEER 119
 QY 121 TRLAKELSLRQKQLAEVEKYKDCDPQVEEIRQANKVAEANKRWTDNIFALKSMA 180
 Db 120 EALBELKAVQDHQHKKEBELAAVADSPALAMMDALVHAALANRWTDNIFLQOWC 179
 QY 181 KRKGFEEENKIDRTF--GIPEPDYID 204
 Db 180 STTFPQAKELHLYTAGITEDPDYIE 206

RESULT 8

YAS3 SCHPO STANDARD; PRT; 210 AA.
 ID YAS3 SCHPO
 AC 009713;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DE Hypothetical protein Cl3A11.03 in chromosome 1.
 GN ORFNames=SPAC13A11.03;
 OS Schizosaccharomyces pombe (fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC NCBI_TaxId=4896;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN=972;
 RC MEDLINE=21848401; PubMed=11859360; DOI=10.1038/nature724;
 RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
 RA Sgouros J., Peat N., Hayles D., Baker S., Basham D., Bowman S.,
 RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
 RA Collins M., Connor K., Cronin A., Davis P., Fellows I., Fraser A.,
 RA Gentile S., Goble A., Hamlin N., Harris D., Hider R., Higgs A.,
 RA Holroyd S., Hornsby T., Howarth S., Huckle E.D., Hunt S., Jagsels K.,
 RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
 RA Mooney P., Moule S., Mungall K., Murphy L., Nislett D., Odeli C.,
 RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
 RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,

RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
 RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
 RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
 RA Weljens I., Vanstreels E., Rieger M., Schaefer M., Meller-Auer S.,
 RA Gabel C., Fuchs M., Fritz C., Holzer E., Moesl D., Hilbert H.,
 RA Borzym K., Langer I., Beck A., Lehnach H., Reinhardt R., Fohl T.M.,
 RA Eger P., Zimmermann W., Wedler H., Wambach R., Purrelle B.,
 RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
 RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
 RA Lucas M., Rochet M., Gallardin C., Tallada V.A., Garzon A., Thode G.,
 RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forburg S.L.,
 RA Ceretti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
 RA Shpakovski G.V., Usero D., Barrell B.G., Nurse P.,
 RT "The genome sequence of *Schizosaccharomyces pombe*,"
 RL Nature 415:871-880(2002).
 CC -----
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 CC -----
 DR EMBL: 254096; CAA90804.1; -
 DR PIR: T37610; T37610.
 DR GenedB: Spombe: SPAC13A11.03; -
 DR InterPro: IPR005647; Mnd1.
 DR InterPro: IPR009058; Wing_hlx_DNA_bnd.
 DR Pfam: PF03962; Mnd1; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 210 AA; 24224 MW; FA546F070A37665 CRC64;

Query Match 33.3%; Score 349; DB 1; Length 210;
 Best Local Similarity 41.6%; Pred. No. 9e-14;
 Matches 84; Conservative 36; Mismatches 76; Indels 6; Gaps 5;

QY 5 KGLSAEKRTRMEIFSETKDVFLQKLEKIAPEKGIITAMSVKEVYQSLVDGMDGDCER 64
 DB 4 KGLSLAEKRTRMEIFHSDKDFQLKEVKGSK-KQIVLTQTKVDLQSLVDNINVTKEK 62
 QY 65 IGTSNYYAFAFSKALHARKHKLVELESQSESGKASLQSKI--EKAKIGRCETE-EKT 121
 DB 63 IGTSNYYAFAFSKALHARKHKLVELESQSESGKASLQSKI--EKAKIGRCETE-EKT 122
 QY 122 RLAKLSSLRD-QREQLKAEVEKYKDCDPQVEEIRQANKVAKEAANRWTDNIPAIKSWA 180
 DB 123 QYTLLELHAKSESELKILKTQLSNLHNCNPEFELKKNENTKTYWEAANLWTDQIHLLIAPC 182
 QY 181 KRKGFEEKIDRTGIPEDFD 202
 DB 183 -RDMGADTNQIREYCSIPEDLD 203

RESULT 9
 O8SUA9 PRELIMINARY; PRT; 203 AA.
 AC O8SUA9;
 DT 01-JUN-2002 (TREMBLrel. 21, Created)
 DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE Hypothetical protein ECU10_1600.
 OS Name=ECU10_1600;
 OS Eucephalitozoon cuniculi GB-M1.
 OC Eukaryota; Fungi; Microsporidia; Unikaryoniidae; Eucephalitozoon.
 OX NCBI_TaxID=284813;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=GB-M1;
 RX MEDLINE=21576510; PubMed=11719806; DOI=10.1038/35106579;
 RX Katinka M.D., Duprat S., Cornillot E., Meisenler G., Thamarat F.,
 RA Prensier G., Barbe V., Peyretailade E., Broctier P., Wincker P.,

RA Delbac F., El Alaoui H., Peyret P., Saurin W., Gouy M.,
 RA Weisenbach J., Vivares C.P.,
 RT "Genome sequence and gene compaction of the eukaryote parasite
 RT *Eucephalitozoon cuniculi*,"
 RL Nature 414:450-453(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=GB-M1;
 RA Genoscope;
 RL Submitted (Apr-2001) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AL590443; CAD25881.1; -
 DR InterPro: IPR002114; Hrp_Serp_S.
 DR InterPro: IPR005647; Mnd1.
 DR InterPro: IPR009058; Wing_hlx_DNA_bnd.
 DR Pfam: PF03962; Mnd1; 1.
 DR PROSITE: PS00589; PTS_HRP_SER; UNKNOWN_1.
 KW Hypothetical protein.
 SQ SEQUENCE 203 AA; 23743 MW; DFE33A65A1A28A42 CRC64;

Query Match 32.5%; Score 340.5; DB 2; Length 203;
 Best Local Similarity 35.1%; Pred. No. 2.8e-13;
 Matches 71; Conservative 50; Mismatches 72; Indels 9; Gaps 3;

QY 7 LSAEKRTRMEIFSETKDVFLQKLEKIAPEKGIITAMSVKEVYQSLVDGMDGDCERIG 66
 DB 6 MSLDQKSLILEIIRIGSKSFYQLQELSLGSK-KGIWVNTIKELIQLVDLGLVTAEKVG 64
 QY 67 TSNYYAFAFSKALHARKHKLVELESQSESGKASLQSKI--EKAKIGRCETEERTRLAE 126
 DB 65 TSNLWYAFASBGIIQKKLRCKELMECERMSQDICKRKEVYIENKWSKRYTERELENK 124
 QY 127 LSSL-----RDREQLKAEVEKYKDCDPQVEEIRQANKVAKEAANRWTDNIPAIKSWA 182
 DB 125 LNALKIKEDQRE----ELGKEERTDPIAYDGLVADRKMEDBCRIIDNVIIDYICS 180
 QY 183 KRKGFEEKIDRTGIPEDFDYI 204
 DB 181 KRPMKESERNSESGIIPDLDI 202

RESULT 10
 O6WDA3 PRELIMINARY; PRT; 203 AA.
 AC O6WDA3;
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE Mnd1.
 OS Giardia lamblia (Giardia intestinalis).
 OC Eukaryota; Diplomonadida; Hexamitidae; Giardinae; Giardia.
 OX NCBI_TaxID=5741;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ramesh M.A., Malik S.B., Logsdon J.M. Jr.,
 RL Submitted (Apr-2003) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AY295092; AA024512.1; -
 DR InterPro: IPR005647; Mnd1.
 DR InterPro: IPR009058; Wing_hlx_DNA_bnd.
 DR Pfam: PF03962; Mnd1; 1.
 SQ SEQUENCE 203 AA; 23278 MW; CC0625DDC4158C0 CRC64;

Query Match 32.5%; Score 340.5; DB 2; Length 203;
 Best Local Similarity 34.8%; Pred. No. 2.8e-13;
 Matches 70; Conservative 46; Mismatches 84; Indels 1; Gaps 1;

QY 5 KGLSAEKRTRMEIFSETKDVFLQKLEKIAPEKGIITAMSVKEVYQSLVDGMDGDCER 64
 DB 4 KGLSLAEKRTRMEIFHSDKDFQLKEVKGSK-KQIVLTQTKVDLQSLVDNINVTKEK 62
 QY 65 IGTSNYYAFAFSKALHARKHKLVELESQSESGKASLQSKI--EKAKIGRCETEERTRLA 124
 DB 63 IGTSNYYAFAFSKALHARKHKLVELESQSESGKASLQSKI--EKAKIGRCETEERTRLA 122

QY 125 KGLSLRDQREQLKAEVEKYKDCDPQVEEIRQANKVAKAEANRWTDNIFAISKMAKRF 184
 Db 123 KEXIALQVLEBQGRTEFRDLKNDPVAQKLRNTYDLAKQGANLMTDNIPLQKXYMTKL 182
 QY 185 GFENKIDRTFGIEDPDYID 205
 Db 183 QMDKKTVSTALGITGEFDYLE 203

RESULT 11

Q7OTX0 PRELIMINARY; PRT; 203 AA.
 AC Q7OTX0:
 DT 01-MAR-2004 (Tremblrel. 26, Created)
 DT 01-MAR-2004 (Tremblrel. 26, Last sequence update)
 DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
 DE GLP 76 12374 11763.
 OS Giardia lamblia ATCC 50803.
 OC Eukaryota; Diplomonadida; Hexamitidae; Giardinae; Giardia.
 OX NCBI_TaxID=184922;
 RP SEQUENCE FROM N.A.
 RC STRAIN=WB C6;
 RA Morrison H.G., McArthur A.G., Adam R.D., Aley S.B., Gillin F.D., Olsen G.J., Sogin M.L.;
 RT "Draft sequence of the Giardia lamblia genome.";
 RI Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is preliminary data.
 CC EMBL: AACB01000100; EAA38463.1; --
 DR InterPro: IPR005647; Mnd1.
 DR InterPro: IPR005058; Wing_hlx_DNA_bnd.
 DR Pfam: PF03962; Mnd1; 1.
 SQ SEQUENCE 203 AA; 23278 MW; CC0625DCD4158C0 CRC64;

Query Match 32.5%; Score 340.5; DB 2; Length 203;
 Best Local Similarity 34.8%; Pred. No. 2.8e-13;
 Matches 70; Conservative 46; Mismatches 84; Indels 1; Gaps 1;

QY 5 KGLSAEKRTRMEIFSETDVPQLDLEKIAPEKGIATMSVKEVLSVDDGMDCCER 64
 Db 4 KGLSLDQREQLKAEVEKYKDCDPQVEEIRQANKVAKAEANRWTDNIFAISKMAKRF 184
 QY 65 IGSNYYWAPPSKALHARKHKLVELESQSEGSQKASLOKSIIEKAKIGRCETEE 124
 Db 63 IGSNYYWAPPSKALHARKHKLVELESQSEGSQKASLOKSIIEKAKIGRCETEE 122
 QY 125 KGLSLRDQREQLKAEVEKYKDCDPQVEEIRQANKVAKAEANRWTDNIFAISKMAKRF 184
 Db 123 KEXIALQVLEBQGRTEFRDLKNDPVAQKLRNTYDLAKQGANLMTDNIPLQKXYMTKL 182
 QY 185 GFENKIDRTFGIEDPDYID 205
 Db 183 QMDKKTVSTALGITGEFDYLE 203

RESULT 12

Q609F9 PRELIMINARY; PRT; 179 AA.
 AC Q609F9:
 DT 05-JUL-2004 (Tremblrel. 27, Created)
 DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
 DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
 DE MND1 domain containing protein.
 OS Aedes aegypti (Yellowfever mosquito).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Aedes.
 OX NCBI_TaxID=7159;
 RP SEQUENCE FROM N.A.
 RC Tissue=Salivary gland;
 RA Chandra P.K., Mikol S.K.;

RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY552061; AAS79347.1; --
 DR InterPro: IPR005647; Mnd1.
 DR Pfam: PF03962; Mnd1; 1.
 SQ SEQUENCE 179 AA; 20900 MW; 6E0016920350E476 CRC64;

Query Match 31.8%; Score 332.5; DB 2; Length 179;
 Best Local Similarity 37.1%; Pred. No. 7.6e-13;
 Matches 66; Conservative 52; Mismatches 57; Indels 3; Gaps 2;

QY 1 MSK-KKGLSAEKRTRMEIFSETDVPQLDLEKIAPEKGIATMSVKEVLSVDDGMDCCER 59
 Db 1 MSK-KKGLSAEKRTRMEIFSETDVPQLDLEKIAPEKGIATMSVKEVLSVDDGMDCCER 59
 QY 60 VDCENIGSNYYWAPPSKALHARKHKLVELESQSEGSQKASLOKSIIEKAKIGRCETEE 119
 Db 61 VETDKIGSNYYWAPPSKALHARKHKLVELESQSEGSQKASLOKSIIEKAKIGRCETEE 120
 QY 120 RTFLAKESLRDQREQLKAEVE--KYKDCDPQVEEIRQANKVAKAEANRWTDNIFA 175
 Db 121 SSMPEKNTLKEKQKSLKDKAKLKDQNSVDKNNRLPDLDHAAKRWGDTTYS 178

RESULT 13

Q7RH53 PRELIMINARY; PRT; 196 AA.
 AC Q7RH53:
 DT 01-MAR-2004 (Tremblrel. 26, Created)
 DT 01-MAR-2004 (Tremblrel. 26, Last sequence update)
 DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
 DE Homo sapiens GAD, putative.
 GN Name=PY04140;
 OS Plasmodium yoelii yoelii.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporidia; Plasmodium.
 OX NCBI_TaxID=73239;
 RP SEQUENCE FROM N.A.
 RC STRAIN=17XNL;
 RX PubMed=12368865; DOI=10.1038/nature01099;

RA Carlton J.M., Angiolini S.V., Suh B.B., Kooij T.W., Petrea M., Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L., Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L., Shalimov S.J., Van Aken S.E., Riedmiller S.B., Feldblum T.V., Cho J.K., Quackenbush J., Sedegah M., Shoabih A., Cummings L.M., Florens L., Yates F.R., Raine J.D., Sinden R.E., Harris M.A., Cunningham D.A., Preiser P.R., Bergman L.W., Valdivia A.B., van Lin L.H., Jansz C.J., Waters A.P., Smith H.O., Gardner M.J., Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J., Carucci D.J.;
 RT "Genome sequence and comparative analysis of the model rodent malaria parasite Plasmodium yoelii yoelii.";
 RL Nature 419:512-519(2002).
 CC -!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is preliminary data.
 CC EMBL: AABL01001237; EAA15959.1; --
 DR InterPro: IPR005647; Mnd1.
 DR Pfam: PF03962; Mnd1; 1.
 SQ SEQUENCE 196 AA; 23066 MW; 7FD8820707329074 CRC64;

Query Match 26.5%; Score 277; DB 2; Length 196;
 Best Local Similarity 29.7%; Pred. No. 1.9e-09;
 Matches 60; Conservative 52; Mismatches 76; Indels 14; Gaps 3;

QY 3 KKKGLSAEKRTRMEIFSETDVPQLDLEKIAPEKGIATMSVKEVLSVDDGMDCCER 62
 Db 2 KKKGLSAEKRTRMEIFSETDVPQLDLEKIAPEKGIATMSVKEVLSVDDGMDCCER 60
 QY 63 ERIGTSNYYWAPPSKALHARKHKLVELESQSE-----GSQKASLOKSIIEKAKIGRC 115
 Db 61 EKVGSGNVFMILKTESSILQNKQYELDKKEVEEMQAQKENTAELENSIS-----L 114
 QY 116 ETERTRLAKESLRDQREQLKAEVEKYKDCDPQVEEIRQANKVAKAEANRWTDNIFA 175

Db 115 KTDEKDTLKEVKNYLDISIEIKSELDKLTDIRQIEKIKQSNFATESIERMNNIPL 174
 QY 176 IKSMAKRGFEENKIDRTFGI 197
 Db 175 LKQWIDRTKNSGDVDRLLGM 196

RESULT 14

06B0L5 PRELIMINARY; PRT; 211 AA.
 ID 06B0L5
 AC 06B0L5;
 DT 25-OCT-2004 (TREMBlrel. 28, Created)
 DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
 DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
 DE Similar to CA34131IPF9239 Candida albicans IPF9239 unknown function (Fragment).
 GN ORFNames=DEHA0E04994G;
 OS Debaryomyces hansenii CBS767.
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Debaryomyces.
 OX NCBI_TaxID=284592;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CBS767;
 RG Genolevures;

RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S., Lafontaine I., de Montigny J., Marek C., Neuvéglise C., Talla E., Goffard N., Frangul L., Aigle M., Anhouard V., Babouy A., Barbe V., Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C., Boissier A., Boyer J., Catolico L., Confantolero F., de Darvar A., Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Gropi A., Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R., Kerrest A., Kozul R., Lemaire M., Lesur I., Ma L., Muller H., Nicard J.M., Nikolaki M., Oztas S., Ozier-Kalogeropoulos O., Pellenz S., Peltier S., Richard G.F., Straub M.L., Suleau A., Swenne S., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B., Zenou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A., Bouchier C., Caudon B., Scarpelli C., Gaillardin C., Weissenbach J., Winkler P., Souclet J.L.;
 RA "Genome evolution in yeasts."
 RT Nature 430:35-44(2004).
 RL [2]
 RN SEQUENCE FROM N.A.
 RC STRAIN=CBS767;
 RG Genoscope;
 RA Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; CR382137; CAG87731.1; --
 DR InterPro; IPR005647; Mnd1.
 DR Pfam; PF03962; Mnd1; 1.
 FT NON_TER
 SQ SEQUENCE 211 AA; 24831 MW; F8B5DC66618334C8 CRC64;

Query Match 25.5%; Score 266.5; DB 2; Length 211;
 Best Local Similarity 29.0%; Pred. No. 8.8e-09;
 Matches 61; Conservative 55; Mismatches 75; Indels 19; Gaps 5;

QY 4 KKGLSAEKRTMMIEFSETKQVFOQLDKLEIAPKE-KGITAMSVKEVLSQSLVDGNCVCE 63
 Db 3 KKGLSAEDKKEKLYEFNOSHTEFTLKEIEKESKYAKTSSMLIKDIVOOLIDMNLINCE 62
 QY 64 RIGTSNYVYAFPSKALHARKHLEVLSELS--ESGQHASLQKS--IEKAKIGRCET-- 117
 Db 63 KCGITNLVYCF-----KFDKIKTLQTOYNNYQNTLKEKQLEKRDQLEKIQGLQRLV 115
 QY 118 ---EERTLAKELSLRDQREQLKAEVEXYKDCDPQVEEIRQANKVAKAANRWTDNI 173
 Db 116 KSDFGNRHKLIDQFTLSKRLHLEBELLKYGNDNPQLITLDEKRVHILAIETFTDDI 175
 QY 174 FAKSWAKR--KFGFEENKIDRTFGIPEDF 201
 Db 176 ESMIYFTVVSATIEELDRSELGIPSEF 205

RESULT 15

075CH5

ID 075CH5 PRELIMINARY; PRT; 225 AA.

AC 075CH5;

DT 05-JUL-2004 (TREMBlrel. 27, Created)

DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)

DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)

DE ACL056CP.

GN ORFNames=ACL056C;

OS Ashbya gossypii (Yeast) (Eremothecium gossypii).

OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

OC Saccharomycetales; Saccharomycetaceae; Eremothecium.

OX NCBI_TaxID=33169;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=ATCC 10895;

RA Brachet S., Voegelé S.E., Dietrich F.S., Lerch A., Gaffney T.,

RA Philippsen P.;

RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.

DR EMBL; AB016816; AAS51172.1; --

DR AGD; ACL056C; --

DR InterPro; IPR005647; Mnd1.

DR Pfam; PF03962; Mnd1; 1.

SQ SEQUENCE 225 AA; 25753 MW; BA73C889FFBEB90F CRC64;

Query Match 21.1%; Score 221; DB 2; Length 225;

Best Local Similarity 26.4%; Pred. No. 5.3e-06;

Matches 56; Conservative 51; Mismatches 93; Indels 12; Gaps 5;

QY 3 KKGLSAEKRTMMIEFSETKQVFOQLDKLEIAPKE-KGITAMSVKEVLSQSLVDGNCV 60
 Db 4 KAAVTLAEKKARVLPFQEBHSIYSINDLETKIPKCGVSMVVKDIOVLIDBDGHI 63
 QY 61 DCEKIGTSNYVYAFPSKALHARKHLEVLSELSGSGQHASLQKSIF-----KAKIGR 114
 Db 64 SYEKCGNVMVYVCFNKOVLGKMKCTEQAMKARSESQVRLQSLQALINSEKKHARAAFR 123
 QY 115 CTEERTR--LAKELSLRDQREQLKAEVEXYKDC--DPQVEEIRQANKVAKAANRWTDNI 170
 Db 124 SGVSYTRQALTEHDELGRQALQSAVRYKLEDTKMDTKIDSYCRGVRSKLQDLKIT 183
 QY 171 DNIFAISWAKRKGFEENKIDRTFGIPEDF 202
 Db 184 DNIEVIVSFLMRHRAVSRALAAALDMPPEFE 215

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